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June 16, 2004, 19:06:57; Search time 84.1687 Seconds (without alignments) 2265.920 Million cell updates/sec
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1 MPRAQPSSASYQPVPADPFA......KTPIQILGQEPDAEMVEYLI 675
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STIMMARTES

	Description	Aay54052 An angiog	8	Aay54053 A variant	Abp43965 Unidentif	Abp69085 Human pol	Human	Adc38518 Human AML	Human	Mouse	3 Mouse	Human .	Abg97502 Human NOV	Нитап	Abg17959 Novel hum	37657 Human ang	0	4 Anglos	įεĮ	Aab94793 Human pro		Abg15667 Novel hum	71039 Drosophil		Abb61040 Drosophil	Abb63519 Drosophil
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SUMMARIES		AAY54052	AAE37918	AAY54053	ABP43965	ABP69085	AAU69439	ADC38518	ADC37654	ABR56262	ABR56263	AAB41861	ABG97502	AAB92866	ABG17959	ADC37657	AAM93770	AAY54054	ABU70751	AAB94793	ABB57023	ABG15667	ABB71039	ABB60579	ABB61040	ABB63519
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	Aam29234 Peptide # Abb3057 Peptide # Abb21158 Protein # Aam68923 Human bon		Abg38504 Human pep Abu08490 Fragment Abr92087 Human cer Aab35408 Human 07C	Abg20119 Novel hum Abu08487 S. pneumo Abp63024 Human pol	Aab95541 Human pro Abr41356 Human DIT Aab41231 Human ORP
ABR57561 AAM16746 ABB35732	AAM29234 ABB30567 ABB21158 AAM68923	AAM56541 ABG50588 AAM04463	ABG38504 ABU08490 ABR92087 AAB35408	ABG20119 ABU08487 ABP63024	AAB95541 ABR41356 AAB41231
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ALIGNMENTS

AAY54U52	
8	AAYS4052 standard; protein; 675 AA.
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A A	AAY54052;
<u> </u>	27-MaR-2000 (first entry)
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DE	An angiogenesis-associated protein which binds plasminogen.
X	
\$	Human, angiogenesis-associated protein; plasminogen; ABP-1;
₹	kringle domain; angiostatin; plasminogen receptor;
₫.	angiogenesis-related disease; tumor; diabetes; rheumatoid artnritis;
₹ }	inflammatory disease; psoriasis; chronic inflammation; intestine; aschmua;
ž X	obesity; gene therapy.
S	Homo sapiens.
i i	WOODG66738-b1
ž	. 40-05000000
PD	23-DEC-1999.
X I	
à Þ	11-JUN-1999; 99MO-EFFUCALOS.
PR	15-JUN-1998; 98SE-00002130.
PR	15-JUN-1998; 98US-0089266P.
띥	17-DEC-1998; 98SE-00004372.
99.	
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PA	(PHAA) PHAKMACIA & UPUCHN AB.
됩	Holmaren L, Troyanovsky B;
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DR	WPI; 2000-106099/09.
E E	N-PSDB; AAZ45329.
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7 >	סו מואסותבואי
é č	Claim 4: Page 43-46: 5800: English.
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ខ	The present sequence represents a human angiogenesis-associated protein
ខ	which is able to bind an N-terminal fragment of plasminogen. The protei
ខ	is designated ABP-1, and binds the first 4 kringle domains (K1-K4) and/or
S	kringle 5 (KS) of plasminogen. These four kringle domains comprise
ပ္ပ	
ប្ដ	angiostatin-binding domain of the ABP-1 protein is described in AAY54054
Ü	A RO GESCTIONE IN ARISHUSS ABE-I

diseases or disorders, such as tumor conditions, diabetes, rheumatoid arthritis, and even some inflammatory diseases such as psoriasis, chronic inflammation of the intestine, asthma, etc. The protein may also be able to treat and cure, or prevent, obesity. The ABP-1 DNA can be used in gene therapy techniques

ö 180 120 120 180 240 240 300 300 360 VISHSPNISYDTALEARIOKEEBEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRS 360 420 480 480 540 540 600 660 9 420 600 60 9 TNVSEYNAAALMELLREKEERILALEADMIKWEQKYLEENVMRHFALDAAATVAAQRDTT 1 MPRAQPSSASYQPVPADFFAIVSRAQQMVEILSDENRNLRQELEGGYEKVARLQKVETEI ORVSBAYENEVKSSSKRBALEKAMENKLBGEIRRMHDFNRDLRERLETANKOLAEKBYEG ORVSEAYENLVKSSSKREALEKAMENKLEGEIRRMHDFNRDLRERLETANKOLAEKBYBG SEDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKL BEELKKKOVYVDKVEKMOQALVQLQAACEKREQLEHRLRTRLERELESLRIQQRQGNCQP VISHSPNTSYDTALBARIQKEEEEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRS RKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLG GDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAA GDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAA AATAAAITATATITTTMVAAAPVAVAAAAPABAAAAPSPATAAATAAAVSPAAAGQIPA 481 AATAAAITATAATIITTIMVAAAPVAVAAAAAPAAAAPSPATAAATAAAVSPAAAGQIPA aasvasaaavabaaaavovapaaapapvpapalvpvpapaaaaaaaaagasapagtoaptsapa VAPTPAPTPTPAVAQABVPASPATGPGPHRISIPSLICUPDKTDGPVFHSNTLBRKTPIQ 601 VAPTPAPTPTPAVAQAEVPASPATGPGPHRLSIPSLITCNPDKTDGPVFHSNTLZRKTPIQ SEDTRKTI SQLFAKNKBSOREKEKLEAELATARSTNEDORRHI EI RDQALSNAQAKVVKL 1 MPRAQPSSASYQPVPADPPAIVSRAQQMVEILSDBNRNLRQELEGCYEKVARLQKVETEI ö 100.0%; Score 3347; DB 3; Length 675; 100.0%; Pred. No. 1.2e-201; ive 0, Mismatches 0; Indels 0 661 ILGORPDAEMVEYLI 675 661 ildospokemverii 675 Conservative al Similarity 675; Conserv Sequence 675 AA; 61 241 301 601 61 121 181 181 301 361 361 421 421 481 541 Query Match Local Sest Loca

SULT 2 E37918

į AAE37918 standard; protein; 993

AAE37918;

(first entry) 06-NOV-2003

Human CGDD-7 protein

death protein; CGDD; leukaemia; Human; cell growth, differentiation and

muscular disorder; myotomic dystrophy; catatonia; endocrine disorder; diabetes; drave's disease; cancer; immunological disorder; scleroderma; systemic lupus erythematosus; allergy; Crohn's disease; renal disorder; gastrointestinal disorder; doodpasture's syndrome; infection; cirrhoeis; cardiovascular disorder; atherosclerosis; hepatic disease; transgenic; transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic; dermatological; immunosuppressive; cerebroprotective; anticonvulsant; antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant; protozoacide; nootropic.

WG2003050253-A2.

19-JUN-2003

2002WO-US039133. 04-DEC-2002;

07-DEC-2001; 20-DEC-2001; 15-JAN-2002;

2001US-0340747P. 2001US-0342761P. 2002US-0349705P. 2002US-0354764P.

06-FEB-2002;

(INCY-) INCYTE GENOMICS INC.

Ë Tang 1, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
Paughn MR, Gorrad AE, Yue H, Lee EA, Becha SD, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia i, Blake JJ, Ho A, Zheng W; Marquis JP, Tran UK, Swa Sprague WW, Burrill JD, Griffin JA,

2003-532903/50.

N-PSDB; AAD57227

New GGDD polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of GGDD, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.

Claim 1; Page 220-222; 299pp; English.

The present invention relates to novel cell growth, differentiation and death (CGDD) proteins and polynucleotides encoding them. The sequences of the invention are useful in diagnosing, preventing and treating disorders associated with an abnormal expression or activity of CGDD such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), mencular disorders (e.g. quichetes, Grave's disease), cancers (e.g. diabetes, Grave's disease), cancers (e.g. diabetes, Grave's disease), cancers (e.g. diabetes, Grave's disease), cancers (e.g. disorders (e.g. crohn's disease), remaindedisciplination of sorders (e.g. disorders (e.g. diabetes), candiovascular disorders (e.g. datastinal disorders (e.g. diabetes), candiovascular disorders (e.g. datastic), protozoal, helminthic), cardiovascular disorders (e.g. datastic), cand hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to create humanised animals or transgenic animals to model human diseases.

Sequence 993 AA;

0; Gaps 99.5%; Score 3331; DB 7; Length 993; 99.6%; Pred. No. 2e-200; ive 1; Mismatches 2; Indels (Local Similarity 99.6 nes 672; Conservative Query Match

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kringle domain; angiostatin; plasminogen receptor;
angiogenesis-related disease; tumor; diabetes; rheumatoid arthritis;
inflammatory disease; psoriasis; chronic inflammation; intestine; asthma;
           SEDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKL 180
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/note= "these residues are either Glu-Leu-Ala or Thr-Thr-
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Pred. No. 2.9e-200;
0; Mismatches 4; Indels C
                                                                                                                                                                                                                 treating
                                                                                                                                                                                                                                                                         Claim 5; Page 46-49; 58pp; English
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98SE-00002130.
98US-0089266P.
98SE-00004372.
98US-0114386P.
                                                                                              (PHAA ) PHARMACIA & UPJOHN AB
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Best Local Similarity 99.4%;
Matches 671; Conservative
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                                                                                                                                                                                                             rel human protein useful disorders.
                                                                                                                                     Troyanovsky
                                                                                                                                                                          WPI; 2000-106099/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 675 AA;
  15-JUN-1998;
15-JUN-1998;
17-DEC-1998;
29-DEC-1998;
                                                                                                                                     Holmgren L,
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                                                   601 VAPTPAPTPTPAVAQAEVPASPATGPGPHRLSIPSLICNPDKTDGPVFHSNTLERKTPIQ 660 601 VAPTPAPTPAVAQAEVPASPATGPGPHRLSIPSLICNPDKTDGPVFHSNTLERKTPIQ 660
541 AASVASAAAVAPSAAAAAAVQVAPAAPAPVPAPALVPVPAPAAAQQSSAPAQTQAPTSAPA 600
                                                                                                                                                                                                                                                                                                                                                                             Neuroprotective; immunomodulator; cancer; chromosome X; cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer, Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation; vulnerary.
                                                                                                                                                                                                                                              ABP43965 standard; protein; 479 AA
                                                                                                                                                                                                                                                                                                                                               Unidentified protein seguence.
                                                                                                                                            661 ILGQBPDAEMVEYLI 675
                                                                                                                       661 ILGQEPDAEMVEYLI 675
                                                                                                                                                                                                                                                                                                              26-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                               ABP43965;
                                                                                                                                                                                                           SULT 4
P43965
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496 300 556 360

241 PSTPILLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVBAPVAAATAAAITATAATITT

PSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATAATITT

437

557 AAAVQVAPAAPAPAPAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPAVAQA 616

ò 셤 ð

TWVAAAPVAVAAAAAAAAAAAPSPATAAATAAAVSPAAAGQI PAAASVASAAAVAPSAAA

497

EVPASPATGPGPHRLSIPSITCNPDKTDGPVPHSNTLERKTPIQILGQEPDAEMVZYLI 675

617

421

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316 120 376 180 436

61 EKEERILALEADMIKWEQKYLEENVWRHFALDAAAIVAAQRDTIVISHSPNISYDTALEA

EKEBRILALEADMIKWEQKYLBENVWRHFALDAAATVAAQRDTTVISHSPNTSYDTALEA

257

197 MOOALVOLOAACEKREOLEHRLRTRLERELESLRIQOROGNCOPTNVSEYNAAALMELLR 1 MQQALVQLQAACEKREQLEHRLRTRLERELESERIQQRQGNCQPTNVSBYNAAALMELLR 377 KSIMSISNAGSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVP 181 KSIASISNAGSGLISHSSTUTGSPINEEKRDDKSWKGSLGILLGGDYRABYVPSTPSPVP

RIQKEEEEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKBPSKTEQLSCMRPA

317

ABP69085 standard; protein; 637 20-JAN-2003 (first entry) ABP69085;

Ren F;

Zhao QA,

Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Xue AJ, Yang Y, Wehrman T, Drmanac RT;

(HYSE-) HYSEQ INC

WPI; 2002-426278/45. N-PSDB; ABQ61209.

11-OCT-2001; 2001WO-US027760 12-OCT-2000; 2000US-00687527

WO200231111-A2

18-APR-2002

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Human polypeptide SEQ ID MO 1132.

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; parkinson; disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; haemostatic; untidiabetic; immunosuppressive; dermatological; antiarthritic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic.

New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or

05-MAR-2002; 2002WO-US005095 DS-MAR-2001; 2001US-00799451 (HYSE-) HYSEQ INC. WO200270539-A2 Homo sapiens RESULT 5
ABP69085
XX
AC ABP6
XX
XX
BB Huma
BB Huma The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, valinerary, neuroprotective, immunomodulator, cytostatic and antiniflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, autoimmune disorders, cancer or disagnostic and research methods. The sequences given in records ABB43544. ABB4399 represent polypeptides encoded by polynucleotides of the invention. NoTEs The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pot_sequences Claim 20; SEQ ID # 868; 357pp + Sequence Listing; English.

ъ, Zhao QA, 1 Ghosh M; Zhang J, Z| R, Wang Z, Goodrich RW, Asundi V, Zha Ma Y, Yamazaki V, Chen R, J, Wang D, Drmanac RF; Tang YT, Zhou P, G Xue AJ, Yang Y, Ma Wehrman T, Wang J,

WPI; 2002-759812/82. N-PSDB; ABZ11302.

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Gaps

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Length 479;

Ouery Match 71.1%; Score 2381; DB 5; Length 4 Best Local Similarity 100.0%; Pred. No. 3.4e-141; Matches 479; Conservative 0; Mismatches 0; Indels

Ä

Sequence 479

New polynucleotides comprising sequences assembled from expressed

sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.

English. ID NO 1132; 1012pp + Sequence Listing; The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ1056) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP66902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Albreimer's diseases (multiple sclerosis, diabetes, lupus) genetic disorders, well or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or iung fibrosis, infections (Dacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did out form part of the princed specification, but was obtained in electronic format directly from WIPO at fig.whpo.int/published_pot_sequences

Sequence 637 AA;

43.3%; Score 1448; DB 5; Length 637; 62.0%; Pred. No. 1.9e-82; ative 83; Mismatches 82; Indels 14; Gaps Query Match
Best Local Similarity 62.0%
Matches 292; Conservative

9

- 61 2 PRAOPSSASYOPVPADPFALVSRAQOMVBILSDENRNIRQELEGCYEKVARLOKVETEIQ
- 121 62 RVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLABKEYEGS
- 277 122 EDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKLE 181 219 BD-KAAEGHYASQNKZFLKEKEKLEMELAAVRTASEDHRRHIEILDQALSNAQARVIKLE
- 301 NVSEYNAAALMELLREKEERILLALBADMTKWEQKYLBENVMRHFALDAAATVAAQRDTTV 242
- 338 NMPEYNAPALLELVREKEERILALEADMTKWEOKYLEESTIRHFANNAAATAAAERDTTI 397
- 302 ISHSPNTSY-DTALEARIQKEEEEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRS 360
- 515 361 RKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLFGSPIMEEKRDDKSWKGSLGILLG 420
- 421 GDYRAEYVPSTPSPVPPSTPL-----LSAHSKTGSRDCSTQTERGTE 462 516

SULT 6 U69439

AAU69439 standard; protein; 608

AAU69439;

29-JAN-2002

Human purified secretory polypeptide #8.

Human, purified secretory polypeptide, cell proliferative disorder,

cancer; immune system disorder; neurological disorder; mental disorder, motor neuromuscular disorder; central nervous system disorder; enzyme linked immunosorbent assay; ELISA; gene therapy

Homo sapiens.

WO200162918-A2.

30-AUG-2001.

01-FEB-2001; 2001WO-US003465

24-FBB-2000; 2000US-0185215P.
24-FBB-2000; 2000US-0185216P.
16-MAY-2000; 2000US-0205232P.
17-MAY-2000; 2000US-020588PP.
17-MAY-2000; 2000US-020588PP.
17-MAY-2000; 2000US-020588PP.
17-MAY-2000; 2000US-020533P.

(INCY-) INCYTE GENOMICS INC.

Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'ea SA, Amshey S, Dahl CR, Dam TC, Daniels SE, Dufour GE; Plores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF; Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A; Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE;

WPI; 2001-648217/74.

Nucleic acids encoding secretory polypeptides, useful in genetic diagnosis and therapy.

Disclosure; Page 192-193; 237pp; English.

the invention. The polypeptides and their associated polymucleotides can be used in the treatment, prevention and diagnosis of diseases associated with inappropriate secretory protein expression. These diseases include cell proliferative disorders such as atherosclerosis and psoriasis, cancers such as leukaemia and melanoma, immune system disorders such as atherosclerosis and psoriasis, cancers such as leukaemia and melanoma, immune system disorders such as schizophrenia and seasonal affective disorder (SAD), motor neuron disorders such as amyotrophic lateral sclerosis, demyelinating disorders such as multiple sclerosis, central nervous system disorders complementary to the target polymucleotide, under conditions in which a phybridisation complex, is formed, and detecting the presence or absence of the complex. The polymptides may also be used as antigens in the production of antibodies protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the sequences of the invention in samples e.g. by enzyme linked immunosorbent assay (ELISA)

Sequence 608 AA;

9 43.2%; Score 1447; DB 4; Length 608; 62.1%; Pred. No. 2e-82; ive 79; Mismatches 84; Indels 16; Gaps Matches 293; Conservative Similarity Query Match Best Local &

2 PRAOPSSASYOPVPADPFAIVSRAQQMVBILSDENRNIRQELEGCYBKVARLQKVBTBIQ 61

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121 62

189 130

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248
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181
                                                                                                     NVSEYNAAALMELLREKEERILALEADMTKWEQKYLBENVMRHFALDAAATVAAQRDTTV 301
                                                                                                                                                          ISHSPNTSY-DTALBARIQKEEEEILMANKRCLDMEGRIKTIHAQIIEKDAMIKVLQQRS 360
                                                                                                                                                                                                             RKEPSKTEQLSCWRPAKSLMSISNAGSGLLSHSSTLTGSPIMERKRDDKSWKGSLGILLG 420
EDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKLE
               BELKKKQVYVDKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESLRIQQRQGNCQPT
                                                                                                                                                                                                                             GDYRAEYVPSTPSPVPPSTPLL-----SAHSKTGSRDCSTQTERGTE
                        190
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122
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ADC38518 standard; protein; 801 SULT 7

ADC38518;

(first entry)

18-DEC-2003

7

Human AMLPla myosin-tail motif amino acià sequence SEQ ID NO:867.

human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy.

Homo sapiens

WO2003037931-A2.

08-MAY-2003

01-NOV-2002; 2002WO-US035129

01-NOV-2001; 2001US-0334773P

(AMSH) AMERSHAM BIOSCIENCES SV CORP.

Shannon M, Phan T;

WPI; 2003-430501/40.

New isolated nucleic acid molecule encoding a human angiomotin-like protein, useful for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1.

Example 2; SEQ ID NO 867; 172pp; English

The present invention describes the human angiomotin-like protein 1 (AMLP1), human AMLP1 has cytostatic activity, and can be used in gene therapy. The AMLP1 protein, nucleic actid molecules, antibodies, and compositions of the present invention can be used for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1. The present sequence represents a myosin-tail motif amino acid sequence, which is used in an example from the present

Sequence 801 AA;

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ÿ
                                            Gaps
                                        83; Indels 14;
      Length 801;
Query Match
Best Local Similarity 61.8%; Pred. No. 6.9e-82;
Matches 291; Conservative 83; Mismatches 83;
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Š	7	PRAQPSSASYQPVPADPPAIVSRAQQMVEILSDENRNLRQELBGCYEKVARLQKVETEIQ 61
qq	331	:
<i>≿</i> 1		RVSEAYENIVKSSSKERALEKAMRNKLEGEIRRWHDFNRDIRERLETANKQLAEKEYEGS 121
ନ୍ଧ	391 F	ISBAYESLVKSTTKRESLDKAMRNKLEGEIRRLHDFNRDLRDRLETANRQLSSREYEGH 450
<i>&</i>	122 E	EDTRKTISQLFAKNKESQREKEKLEABLATARSTNEDQRRHIBIRDQALSNAQAKVVKLE 181
QQ	451 (GD-KAAEGHYASQNKEFLKEKEKLENELAAVRTASEDHRRHIEILDQALSNAQARVIKLE 509
ĕ	182 E	EBLKKKOVYVDKVEKKOQALVQLQAACEKREQLEHRLKTRLERELESLRIQQRQCNCQPT 241
qq	510 E	EELREKQAYVEKVEKLQQALTQLQSACEKREQMERRIRTWIERELDALRTQOKHGWGQPA 569
δ,	242	NYSEYNAAALMELLREKEERILALEADMTKWEQKYLEENVWRHFALDAAATVAAGRDTTV 301
qq	570 1	
Š	302	15HSPNTSY-DTALBARIQKEEEEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRS 360
QQ	630	
Š	361 F	RKEPSKTEQLSCWRPAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLG 420
Db	690 F	
ò	421	GDYRAEYVPSTPSPVPPSTPLLSAHSKIGSRDCSTQTERGIE 462
qq	748 P	KEHH-EHASAPLLPPPPTSALSSIASITAASSAHAKTGSKDSSTQTDKSAE 197
RESULT 8 ADC37654 ID ADC37654		standard, profein, 869 22
	**	
XX DT 18-DE	18-DEC-2003	3 (first entry)

human, angiomotin-like protein 1, AMLP1, cytostatic, gene therapy, Homo sapiens

Human angiomotin-like protein la SEQ ID NO:3.

WO2003037931-A2

08-MAY-2003.

01-NOV-2002; 2002WO-US035129

(AMSH) AMERSHAM BIOSCIENCES SV CORP 01-NOV-2001; 2001US-0334773P

Phan T; Shannon M, WPI; 2003-430501/40. N-PSDB; ADC38522, ADC38523.

New isolated nucleic acid molecule encoding a human angiomotin-like protein, useful for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1.

Claim 14; SEQ ID NO 3; 172pp; English

The present invention describes the human angiomotin-like protein 1 (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and

2003-571281/54.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 RKBPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRODKSWKGSLGILLG 420
                                                                                                                                          61
compositions of the present invention can be used for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1. The present sequence represents human AMLP1a from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; JEAP; Junction-Enriched and Associated Protein; tight junction; exocrine gland; pancreas; submandibular gland; lacrimal gland; parotid gland; sublingual gland.
                                                                                                                                                                                        RVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEGS
                                                                                                                                                                                                                                                         PRAQPSSASYQPVPADPPAIVSRAQQMVEILSDENRNLRQBLEGCYEKVARLQKVETEIQ
                                                                                                                                                                                                                                                                                                                                                                                        302 ISHSPNTSY-DTALEARIOKEEESILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRS
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 GDYRAEYVPSTPSPVPPSTPL-----LSAHSKTGSRDCSTQTERGTE
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                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Junction-Enriched and Associated Protein, JEAP
                                                                                      Query Match
43.1%; Score 1441; DB 7; 3
Best Local Similarity 61.8%; Pred. No. 7.7e-82;
Matches 291; Conservative 83; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morimoto K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABRS6262 standard, protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asano M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BISA ) EISAI CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takai Y;
                                                                Sequence 869 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                        62
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R56262
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The present sequence is the protein sequence for murine Junction-Enriched and Associated Protein (JEAP). JEAP is expressed specifically at tight junctions in exocrine glands such as the pencreas, submandibular gland, lacrimal gland, parotid gland sublingual gland. JEAP is useful for identifying substances which affect its expression, activity or
                                                                                                                                                                                                                                                                                                                                                                                                               392
                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
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                                                                                                                                                                                                                                                                                                                                                                                                   292 TVAAQRDTTVISHSPNTSY-DTALEARIQKEEBEILMANKRCLDMEGRIKTLHAQIIEKD
                                                                                                                                                                                                                                                                                                                                                                                1 MPRAQP-SSASYQPVPADP-----FAIVSRAQQMVBILSDBNRNLRQELEGCYEKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 RLOKVETEIORVSBAYENLVKSSSKREALBKAMRNKLEGEIRRMHDFNRDLRERLETANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLAEKEYEGSEDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 QLSSREYDGHED-KAARSHYVGQNKEFLKEKEKLEMELAAVRTASEDHRRHIBILDQALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAQAKVVKLEEELKKKQVYVDKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESLRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWKGSLGILLG----GDYRABYVPSTPS---PVPPSTPLLSA-HSKTGSRDCSTQTERGT
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                                 New junction-enriched and associated protein 2 which is expressed specifically at tight junctions in exocrine glands, useful for identifying substances which affect the expression, activity or
                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine, JBAP-2; Junction-Enriched and Associated Protein-2; exocrine gland; pancreas; submandibular gland; lacrimal gland; tight junction.
                                                                                                                                                                                                                                                                                                            Length 882;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                            Score 1400; DB 7; ;
Pred. No. 2.9e-79;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein-2,
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                                                                                                                   Claim 13; Page 15-17; 31pp; English
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                                                                                                                                                                                                                                                                                      41.8%; Scor. 58.2%; Pred
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                                                                                  distribution of the protein.
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                                                                                                                                                                                                                                                                                                                                             299; Conservative
                                                                                                                                                                                                                                                                                                                             Similarity
N-PSDB; ACC70742
                                                                                                                                                                                                                                                                         Sequence 882 AA;
                                                                                                                                                                                                                                        distribution
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Mus musculus. 21-MAY-2003.

15-NOV-2002; 2002EP-00079841.

16-NOV-2001; 2001JP-00352241

(BISA) EISAI CO LTD

Ono Y, Morimoto K, Takeuchi M, Inoue Y; Asano M, Nishimura M, Asar Imai T, Takai Y;

2003-571281/54. N-PSDB; ACC70743. New junction-enriched and associated protein 2 which is expressed specifically at tright junctions in exocrine glands, useful for identifying substances which affect the expression, activity or distribution of the protein.

Claim 1; Page 20-22; 31pp; English.

The present sequence is the protein sequence for murine Junction-Enriched and Associated Protein-2 (JEAP-2). JEAP-2 is expressed specifically at tight junctions in exorrine glands such as the pancreas, submandibular gland and lactimal gland. JEAP-2 is useful for identifying substances which affect its expression, activity or distribution

Sequence 772 AA;

Gaps 51, DB 7; Length 772; 32.6%; Score 1090.5; DB 7; Length 50.4%; Pred. No. 6.6e-60; ive 71; Mismatches 118; Indels Conservative Similarity Query Match Best Local Simi Matches 244;

22 PSSFGPPAVEGPPSAQATLGSAELAQMETVLRENARLQRDNERLQRELESTSEKAGRIEK 6 PSSASYQPVPADPFAIV----SRAQQMVEILSD-----ENRNLRQBLEGCYEKVARLOK

284

TGTLAGGGGSHGGSAELSALRLSEQLREKERQILALEADWTKWEQKYLEERAPRQPAMDA 583 ----GNCQPTNVSEYNAAALMELLREKBERILALEADMTKWEQKYLEBNVMRHFALDA 236

289

636

676

AAVA 470 ACLA 735 467

732

RESULT 11 AAB41861

AAB41861 standard; protein; 849 AA.

AAB41861;

(first entry) 08-FEB-2001 Human ORFX ORF1625 polypeptide sequence SEQ ID NO:3250.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; untherary; antipacitatic; antiparkinsonian; nootropic; neuroprotective; antioconvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiarianmanic; gene therapy; cancer; proliferative disorder; hypotrension; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; cardiovascular disease; diabetes mellitus; yraft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe condined immunodeficiency; malaria; autoimmune disorder; astbma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; burnerings thrombosis; contraceptive

Homo sapiens.

W0200058473-A2

05-OCT-2000.

31-MAR-2000; 2000WO-US008621

99US-0127607P. 99US-0127636P. 99US-0127728P. 30-MAR-2000; 2000US-00540763 31-MAR-1999; 02-APR-1999; 05-APR-1999;

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343

Shimkets RA, Leach M;

WPI; 2000-602362/57. N-PSDB; AAC76070.

× Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

Claim 11; Page 2453-2455; 5507pp; English.

AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepacotropic; vulnerary; antiparatial antiparatiansonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiparthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antilinflabetic; impunosuppressive; antilinflabetic; hypotensive; cardiant; thrombolytic; cadgulant; vasotropic; antidabetic; hypotensive; cardiant; thrombolytic; antithyroid; and antianaemic. The cardiant; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, national energy cardiavascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester chicage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cardiary and antinidate damage, noctural hemoglopinuria, antinidamatory disease; to emhance coagulation; to inhibit thrombosis; and as a contraceptive S

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Gaps 10;
                                                                                                                                                             424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           755 SSSERQTADAPARLTTADRAPTEEPVVTAPP--AAHAKHGSRDGSTQTDGPPDSTSTCL- 811
                                                                                                                           63
                                                                                                                                                                                                                   SODWVAKLIAQSYBQQQBQEKLEREMALIRGAIBDQRRRABELLEQALGNAQGRAARABEE
                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGGSPELGALRLSBQLREKEEQILALEADMTKWEQKYLEERAMRQFAMDAAATAAAQRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PVPADPFAIVSRAQQMVEI-----LSDENRNLRQELBGCYEKVARLQKVETELQRV
                                                                                                                                                                                                                                                                TRKTISQL?AKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKLEEE
                                                                                                                                                                                                                                                                                                                                       LKKKKOVYVDKVBKMQQALVQLQAACEKREQLEHRLRTRLERELESLRIQQRQ-----GNC
                                                                                                                                                                                                                                                                                                                                                                                                           239 OPTWVSEYNAAALMELLREKEERILALEADMIKWEOKYLEENVMRHFALDAAATVAAQRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMBEKRDDKSWKGSLGIL
                                                                                         65
                                                      DB 3; Length 849;
                                                  31.1%; Score 1040.5; DB 3; Length 46.6%; Pred. No. 1e-56; ive 80; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PPEPDSLLGCSSSQRAASLDSVATS 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 APISVPAP-----VAAAATAAAITATAAT 493
                                              Query Match
Best Local Similarity 46.67
Matches 237; Conservative
{
} Sequence 849 AA;
                                                                                                                                                                                           64
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ABG97502 standard; protein; 467 AA 3697502

ABG97502;

(first entry) 16-DBC-2002

Human NOVX21 protein.

Hodgkin disease; Von Hippel-Lindau syndrome, Alabieiner; disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain, obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; inflammatory bowel disease; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; accertain infection; arastic infection; graft-versus-host disease; cell differentiation; cell proliferation; haematopolesis; wound healing; angiogenesis; single nucleotide polymorphism; SNP. Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction;

Homo sapiens

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/note= "Asp substituted by Glu as the result of a single nucleotide polymorphism {SNP}"
Location/Qualifiers
                       misc_difference
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14-VAR-2001) 2001US-0276000P.
20-WAR-2001) 2001US-027523P.
20-WAR-2001) 2001US-027732P.
20-WAR-2001) 2001US-027733P.
21-WAR-2001) 2001US-027733P.
22-WAR-2001) 2001US-027731P.
23-WAR-2001) 2001US-0278894P.
27-WAR-2001) 2001US-0278894P.
27-WAR-2001) 2001US-0278894P.
28-WAR-2001) 2001US-0278033P.
02-APR-2001) 2001US-028023P.
02-MAY-2001) 2001US-0280823P.
03-MAY-2001) 2001US-0280823P.
04-MAY-2001) 2001US-0280821P. 2001US-0274849P. 2001US-0275235P. 2001US-0275579P. 2001US-0275601P. 2002WO-US007283 07-MAR-2002; 2002US-00094466 13-MAR-2001; 2 13-MAR-2001; 2 14-MAR-2001; 2 20-MAR-2001; 2 08-MAR-2002;

r UM, Gerlach VL; Kekuda R, Pena CEA; Vernet CA, Tchernev VT, Malyankar UM, usen BD, Patturajan M, Gusev VY, Keku angolli EA, Taupier RJ; Zerhusen BD, Pa I, Gangolli EA, Spytek KA, Shong M,

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WPI; 2002-713508/77. N-PSDB; ABS78746.

multiple New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or Parkinson's disease.

Claim 1; Page 148-149; 266pp; English.

The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, conference of sociated diseases. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, thurtington's disease, cerebral hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, Lesch-Nyhman syndrome, multiple sclerosis, ataxia—telangisctaemia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, athersoclerosis, hypertension, celeroderma, heemophilia diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencise, HIV, viral, bacterial or parasitic nifertiling, and see used as targets for the identification of small colles that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and amplement modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and immunospecifically to NOVX substances for use in therapoutic or diagnostic methods: The nucleic acids are further used as hybridisation pharmacogenomics. The present amino acid sequence represents a human NOVX protein of the invention

Sequence 467 AA;

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130
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                                                                                                                                                                                                             92 IRRMHDPNRDLRERLETANKOLAEKEYEGSEDTRKTISOLFAKNKESOREKEKLEAELAT
                                                                                                                                                ARSTNEDORRHIEIRDOALSNAQAKVVKLEBELKKKKOVYVDKVEKMQQALVQLQAACEKR
                                                                                                                                                                                                                                                         EQLEHRIRTRIERELESIRIQQRQ-----GNCQPTNVSEYNAAALMBLIREKEERILALE
                                                                                                                                                                                                                                                                                                                      ADMIKWEQKYLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEBBEIL
                                                                                                                                                                                                                                                                                                                                           SGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPS-----TPSPVPP
                                                                LSDENRNLRQELEGCYEXVARLQKVETBIQRVSEAYBNLVKSSSKRRALBKAMRNKLEGE
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy
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                                26;
   Length 467;
31.0%; Score 1037; DB 5; Length 46
48.4%; Pred. No. 8e-57;
ive 75; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yi
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:11448
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00183767.
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                al Similarity 48.45
233; Conservative
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S 454
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   Query Match
Best Local
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                                 Matches
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The present invention describes primer sets for synthesising 5602 full-

[ leigth cDNAs defined in the specification. Where a primer set comprises:

[ (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 1'-end sequence. Oscaplementary to a polynucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence. Oscaplementary to a polynucleotide which comprises a 1'-end sequence, where the opinion of the primer sets can be used in antisense therapy and in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the pertent and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the comprise as a saily without any specialised methods. AAH13612 tepresent thuman amino acid sequences; and AAH13622 to AAH13612 represent thuman amino acid sequences; and AAH13622 to persente the complement the exemplification of the company in the exemplification of the company is made to the company of the company in the exemplification of the company in the exemplification of the company is made to the company in the company in the company is made to the company in the company in the company is made to the company in the company in the company is made to the company in the compa
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           Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 OPTNVSBYNAAALMELLREKEBRILALBADMTKWEOKYLEENVMRHFALDAAATVAAORD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 706;
                                                                                                                           Claim 8; SEQ ID NO 11448; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 987.5; DB 4; Length 7; Pred. No. 1.7e-53; 65; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 706 AA;
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ADC37657 standard; protein; 562
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                                                                RESULT 15
ADC37657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) as useful in gene therapy techniques to restore normal activity of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Aggionio-Aggiogna represent novel human diagnostic mainto acid sequences. Aggionio-Aggiogna, represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at five specification, but was obtained in fip. wipo int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SEDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ORVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645 SEDTRKTISQLFAKUKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKL 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 48318; 103pp; English.
                     Novel human diagnostic protein #17950.
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                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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Best Local Similarity 99.5
Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                               WO200175067-A2
                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes the human angiomotin-like protein I (AMLPI). human AMLPI has cytostatic activity, and can be used in gene therapy. The AMLPI protein, nucleic acid molecules, antibodies, and compositions of the present invention can be used for treating or preventing a disorder associated with decreased or increased expression or activity of AMLPI. The present sequence represents human AMLPIb from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PRAQPSSASYQPVPADPPAIVSRAQQMVBILSDBNRNLRQBLEGCYEKVARLQKVBTBIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKBYEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 EDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIBIRDQALSNAQAKVVKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid molecule encoding a human angiomotin-like protein, useful for treating or preventing a disorder associated with decreased or increased expression or activity of AMLP1.
                                               numan; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
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Human angiomotin-like protein 1b SEQ ID NO:6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 6; 172pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
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                                                                                                                                                                                                                                                                                          01-NOV-2002; 2002WO-US035129.
                                                                                                                                                                                                                                                                                                                                            01-NOV-2001; 2001US-0334773P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADC37655, ADC37656.
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Best Local Similarity 65.5%
Matches 152; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-430501/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 562 AA;
                                                                                                                                                                                       WO2003037931-A2
                                                                                                                                       Homo sapiens.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

June 16, 2004, 19:08:12; Search time 28.0562 Seconds (without alignments) 1242.060 Million cell updates/sec protein - protein search, using sw model no c

3347 1 MPRAQPSSASYQPVPADPFA.....KTPIQILGQBPDAEMVBYLI 675 US-09-332-063-2 :le: :fect score: |uence:

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Issued Patents AA:*

1: /cgn2 = 6/ptodate/2/iaa/5A_COMB.pep:*

1: /cgn2 = 6/ptodate/2/iaa/5B_COMB.pep:*

2: /cgn2 = 6/ptodate/2/iaa/6A_COMB.pep:*

4: /cgn2 = 6/ptodate/2/iaa/6B_COMB.pep:*

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6: /cgn2 = 6/ptodate/2/iaa/PGTUS_COMB.pep:*

6: /cgn2 = 6/ptodate/2/iaa/PGTUS_COMB.pep:* :abase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1 4	,	3		H	55	4	m	۲۲ ۵	-	equence 33	v.	equence 184	٠Ĩ	equence 1, Api	equence 7502, A	equence 52,	App		Ļ	Ļ	5	51,	2	21	Sequence 3, Appli	ď	Sequence 18387, A
	QI QI		-08-714	US-08-714-741-32	US-09-579-181-2	9-1	US-09-252-991A-22853	4	US-09-103-429A-3	-188B-1	1-4	US-09-252-991A-32957	US-08-328-254-6	7	US-08-353-700-1	PCT-US95-16216-1	US-09-489-039A-7502	-08-834-306-5	US-08-993-674A-52	US-09-256-976-52	US-08-403-379A-1	4	US-08-557-309B-51	US-08-834-306-51	US-08-993-674A-51	US-09-256-976-51	US-08-875-435B-3	US-09-095-443-2	US-09-252-991A-18387
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3, Appli	31, Appl	54, Appl		-	85, Appl	12, Appl	1, Appli	3, Appli	4, Appli	4, Appli	47, Appl	5273901	5482709	2, Appli	2, Appli	н.	6, Appli
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Patent No.	Patent No.	Sequence	Sequence	Sequence	Sequence
US-08-899-595-3	US-09-595-684B-31	US-08-557-309B-54	US-09-080-897-2	US-09-323-735-2	US-09-154-750A-85	US-09-665-479A-12	US-09-310-187A-1	US-08-938-105-3	US-08-195-487-4	PCT-US93-06160-4	US-09-616-289-47	5273901-7	5482709-6	US-08-533-306A-2	US-08-742-923A-2	US-08-533-306A-6	US-08-742-923A-6
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209.5	209.5	209	208.5	208.5	207	207	206.5	205.5	204	204	203.5	203	203	203	203	203	203
28	29	30	33	33	33	34	35	36	37		39	40	4.1	4	4.	44	4. RJ

ALIGNMENTS

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APPLICANT: Briles, David E.
APPLICANT: Briles, Larry S.
APPLICANT: Swiatle, Larry S.
APPLICANT: Swiatle, Edwin
APPLICANT: Swiatle, Edwin
APPLICANT: Verher, Janet
APPLICANT: Tarr, Rebecca
APPLICANT: Brooks-Walter, Alexis
APPLICANT: Brooks-Walter, Alexis
APPLICANT: Brooks-Walter, Alexis
APPLICANT: Tarra OF INVENTION: EXPRESSION PRODUCTS THIREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
ANDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STREET: OUTLY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IPP C COMPACIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/714,741
FILLING DATE: 16-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-312
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1231 amino acids
                                        Sequence 41, Application US/08714741
Patent No. 6500613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
STRANDESNESS: single
NOLECULE TYPE: amino acid
US-08-714-741-41
RESULT 1
US-08-714-741-41
```

Length 1231;

DB 4;

Score 275;

8.2%;

Query Match

3est Local Similarity 22.3%; Pred. No. 4.5e-10;
4atches 144; Conservative 94; Mismatches 237; Indels 172; Gaps 24; 236 VKAAKDAADKMIDEAKKREBEAKTKENTVRAMVVKEABIELVKEE-----ANBSRNEEKI 290 194 VEKMQQALVQLQAACEKRB-----QIEHRLRTRLERELESLRIQQ-----RQGNCQP 240 241 TNVSEYNAAALMELLREKBERILALBADMTKWE-----QKYLEBNVMRHFALDAAATVA 294 | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 82 KAMRNKLE---GEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKTISQLFAXNKES 138 139 OREKEKLEAELATARSTNEDORRHIEIRDOALSNAQAKVVKLEEELKKKOVYVD----K 193 | : | | ::| | : | :| 462 LQSKLDTKKANLSKLEELSDKIDELDAEIAKLEVQLSSSEDYAKEGF------ 508 295 AQRDITVISHSPNTSYDTALEARIQKEEERILMANKRCLDMEGRIKTLHAQIIEKDAMIK 354 355 VLQQRSRKEPSKTEQLSCWRPAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDKSWKGS 414 415 LGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISV 474 475 PAPVAAAATAAAITATAATIITTIMVAAAPVAVAAAAAAAAAAAAAAAAAAAAAAAAAS 535 AGOIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPAPAPAPAAAVPAPAAAQASAPAQTQA 594 662 APEKPAP-----APEKPAPATPAP-BAPATPAP- 662 APEKPAPAPAPAPKPEK- 710 617 ----TIAAKKAELEKTEADLKK-----AVNEPEKPAPAPEPAP---APSKPABKPAP 661 22 VSRAQQMVBILSDENRNLRQELBGCYBKVARLQKVBTBIQRVSEAYBNLVKSSSKRBALE 81 595 PTSAPAVAPTPAPT-------PTPAVAQ-AEVPASPATG 625 711 ----PAEQPKPEKTDDQQAEBDYARRPEKPAPAPEKPAPTPEKTG 753

DO

SGULT 2

1-08-714-741-32

Sequence 32, Application US/08714741

Patent No. 6500613

GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: Swiatlo, Edwin
APPLICANT: Swiatlo, Edwin
APPLICANT: Toth, Marilyn J.
APPLICANT: Tark, Warilyn J.
APPLICANT: Tark, Marilyn J.
APPLICANT: STREESION PRODUCTS
TITLE OF INVENTION: EXPRESSION PRODUCTS
TITLE OF INVENTION: EXPRESSION PRODUCTS
TITLE OF INVENTION: Marils & Safford, P.C.
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Curtis, Morris & Safford, P.C.
CONTRY: U.S.
ZIP: 10036
COMPUTER READABLE FORM:

COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/714,741 FILING DATE: 16-SEP-1996 CLASSIFICATION: ASP-1996 ATTORNEY/AGENT INFORMATION: NAME: Prommer Esq., William S. RAGISTRATION NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 25,506 REFERENCE/COMPUTICATION INFORMATION: TELEPHONE: (212) #40-333 TELEPHONE: (212) #40-333 TELEPHONE: (212) #40-332 INFORMATION FOR ESQ. ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: #991 amino acid STRANDEDNESS: single STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: amino acid	Query Match 7.9%; Score 263; DB 4; Length 8991; Best Local Similarity 19.3%; Pred. No. 3.4e-08; Matches 164; Conservative 83; Mismatches 298; Indels 306; Gaps	2 PRAQPSSASYQPVPADPFALVSRAQQMVELLSDENRNLRQELEGCYEKVAR : : : : : : : : : : : : : : : : : : : : : : : : : : : :	53 LQKVETEIQRVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDENRDLREKLETANKC		113 LAEKHYEGSEDTRKTISQLFAKUKESQREKEKLEAELATARSTNEDGRRHIEIRUGALSN	173 AQAKVVKLEEELKKKQVYVDKVBKMQQALVQLQAACEKREQLEHRLRTRLERELESI 	5461 PQPEKPABETPAPKPEKPABQPKABKPADQQABEDYAKRSBEBYNKLTQQ 233 OBOGNOODTNYSEVNABARIMETIBEVEDDITAT BANKFKEROKYI FFNIMBH	; ; ; ; ; ; ; ; ; ;	285 FALDAAATVAAQRDTTVISHSPNTSYDTALBARIQKBEEBILMANKRCLDMBGRIKTLHA	S557 -GADPEADIAARPNELAAKQAELAQKPTGLEKLLDSLDPGGKTQ	345 QIIEKDAMIKVLQORSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGS -	400 PIMBEKRDDKSWKGSLGILLGGDYRABYVPS	: : : :	431PSTPLPSTPL	5712 PAPKPEQPAPAPKDEQPAPAPKPEQPAKPEKPABEPTQPEKPATPKTRVRALKVAEFGVQ	442BSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAA	5772 LRDAGGSNNVGÁYFKEĞLEETTARXÉAĞLGKAEADLKKAVDEPETFAPAPAPAPAPAPAP	482 ataaaitatatittimvaaapvayaaaaapsaapspataaataavspaaggipaa	5832 APKDAPAPKPAPAPAPAPAPAPKPAPAPKPAPAPAPAP	542 A
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 PLAPMAAPQTAILAPSPAPPLAPLPVLAPSPGAAPVLASSQTPVPVMAPSSTPGTSLASA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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                                                                                                                                                475
5879 APKPETPKTLKDIDESDSBDYAKEGLRAPLQSELDTKKAKLLKLEELSGKIEBLDABIKE 5938
                                                                                                             561 QVAPPAPAPAPVPAPALVPVPAPAAAQASAPAQTOAPTSAPAVAPTPAPATPAVAQABVPA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ADVAAAA------TAAAIT---ATAATITTIMVAAAPVAVA--- 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----naaapaabapapapataaataaavspaaagoipaaasvasaaaavapsaaaaav 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 QVAP-AAP-----APVPAPALVPVP-----APAAAQASAPAQTQAPTSAP-----AV 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 APTPAPTP--TPAVAQAEVPASPATGPGPHRLSIPSLITCNP--DKTDGPVFHSNTLERKT 657
                                                                        5939 LEVQLKDAEGNNNVEAYFKEGLEKTTAEKKAELEKAEADLKKAVDEPETPAPAPAPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SPEET
FILE REFERENCE: 16153-4247
CURRENT FILING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-27
FRIOR PILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 252; DB 4; Length 29
30.5%; Pred. No. 4.6e-08;
tive 34; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 STPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTA-AVAPISVP
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Patent No. 6365372
GENERAL INFORMATION:
APPLICANT: Yaciuk, Peter
                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09579181
Patent No. 6365372
GENERAL INFORMATION:
                                                                                                                                                                                                                                  6059 PAPAPAPAPK 6069
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les 98; Conservative
                                                                                                                                                                                               621 -SPATGPGPHR 630
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-09-579-181-1
                                                                                                                                                                                                                                                                                                                 -09-579-181-2
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Best Local S
Matches 98
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Sequence 22853, Application US/0925291A

Sequence 22853, Application US/0925291A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION:

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22853

LENGTH: 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 -----alarpaarapspataartraavspaaagqipaaasvasaaavapsaaaaav 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602 APTPAPTP--TPAVAQAEVPASPATGPGPHRISIPSLITCNP--DKTDGPVFHSNTLERKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 -----APVAAAA-----TAAAIT---ATAATITTIMVAAAPVAVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 96;
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SNF2 Related CBP Activator Protein (SRCAP)
                                                                                                                                                                                                                                                                                                                                               7.5%; Score 252; DB 4; Length 3118; 30.5%; Pred. No. 4.9e-08; tive 34; Mismatches 103; Indels 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 STPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTA-AVAPISVP
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7.5%; Score 250.5;
Best Local Similarity 25.4%; Pred. No. 4.66
Matches 107; Conservative 42; Mismatches
                          FILE REFERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1592 GNPQGPPPTQTLSLTPASSLV 1612
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                           Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                       98; Conservative
                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 1
LENGTH: 3118
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-22853
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                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Fuman
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MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: APPLICATION WHERE: US/09/103,429A FILING DATE: 24-JUN-1998 ATTORNOV.ACTION 1800
TISSUE TYPE: peritrophic membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INPORMATION:
NAME: Michaels, Christopher A
RECISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-39
TELECOMUNICATION INPORMATION:
TELEPHONE: (607) 256-2000
                                                                                                                                                                                                                                                                                                                                                                 589 PAOTOAPISAPAVAPIPA----
                                                                                                            427 YVPSTP---SPVPPSTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (60) 256 3628
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 786 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                701 TPEDĎDIĎPPL 711
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STRANDEDNESS: single
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                                                             Best Local Similarity
Matches 90; Conserv
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US-09-103-429A-4
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                                                                                                                                                                                              452 DCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITA-TAATITTTMVAAAPVAVAAAA 510
                                                                                                                                                                                                                       511 APAAAAAPSPATAAATAAAVSPAAAGOIPAASVASAAAAAPSAAAAAAAVQVAP----AA 566
                                                                                                                                                                                                                                                                                        271 paaktaarpaakpaakpvakétak---paaktaaakpaakpaakpaakpaakpvaksaa 327
                                                                                                                                                                                                                                                                                                                                                  -----VKTVAAKPAAKPAAKPAAKPAAKPAA- 223
                                                                  332 CLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLS 391
                                                                                                                               392 HSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSR 451
     272 WEÇKYLEENVWRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIÇKEBEBILMANKR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4. Application US/09103429A
Sequence 4. Application US/09103429A
Selent No. 618755B
GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Granados, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: A No. 6187558el Envertebrate OF INVENTION: A NOT TITLE OF INVENTION: A NOT TITLE OF INVENTION: A CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: Ithaca
SITREET: OF SECURATION: A NO. 6187558th Tioga
CITY: Ithaca
                                                                                        ORGANISM: Trichoplusia ni
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641 bapnitutapptaapttaapapnitutupptaaptaapptuahapnitaaputtisabat 700
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                                                                                                                                                                                                                                                      458 ------ERGIESNKTAAVAPISVPAPVAAATAAAITATAATI----ITTWVAAA 502
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                                                                                                                            ----STOT 457
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                                                                   Gaps
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Sequence 3, Application US/09103429A
Sequence 3, Application US/09103429A
Sequence 3, Application US/09103429A
GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin TITLE OF INVENTION: CDNA and Related Products and Methods NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6187558th Tioga
7.1%; Score 237.5; DB 3; Length 805; illarity 28.9%; Pred. No. 8.1e-08; Conservative 21; Mismatches 107; Indels 93
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307 NTSYDTALEARIQKEEBEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSK 366
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                                                                                    307 NTSYDTALBARIOKERBRILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSK 366
                                                                                                                                       ---ORQLEI---- 431
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                                                                                                                                                                                                                                                       367 TEQLSCHRPAKSLMSISNAGSGLLSHSSTLTGSPIMBEKRDDKSWKGSLGILLGGDYRAE
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                                                                                                                                                                                                                                                                                                                    544 --PPIPQASPGPPG-PL---SQTPPMQRPVEPQEGPHKSLVAHRVPLK---PYAAPVPR
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APPLICANT: PLOMMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: 0509/291,417D
CURRENT PILING DATE: 1999-04-13
PRIOR PILING DATE: 1998-04-14
PRIOR PILING DATE: 1998-04-14
SEQ ID NO SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 155
    -----MQALRREBERROA-----EREQEYIRHRLEEB-
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Best Local Similarity 21.75
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 CESPVTAGCOVFECDSDNOCTSTAAPTAAPTAAPTAAPTAAPTAAPSTVVPPATPPATAA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ERGTESNKTAAVAPISVPAPAAAATAAAITATAATI---TTTMVAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVAVAAA----AAPAAAAPSPATAA---ATAAAVSPAAAGQIPAAA----SVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    547 AAAVAPSAAAAAVQVAPAAPAP------VPAP-ALVPVPAPAAAQASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           524 PVPPTTAIPTPAPTAAPTAAPTAAPESPITVTVPPTAA---PTAAPTTAVPBIPITVTS
                                                                                                                                                                                                                                                                                                                                                                   Gape
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                                                                                                                                                                                                                                                                                                                                                                   90;
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                                                                                                                                                                                                                                                                              Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LLSAHSKTGSRDC-
                                                                                                                                                                                                                                                                     7.0%; Score 235; DB 3; Length 78 ilarity 30.0%; Pred. No. 1.2e-07; Conservative 20; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOWANN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION: SYE2O-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR APPLICATION NUMBER: 60/291,417
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR RILING DATE: 1999-04-14
PRIOR RILING DATE: 1999-04-14
              ANTI-SENSE: NO ORIGINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Trichoplusia ni TISSUE TYPE: peritrophic membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 YVPSTP---SPVPPSTP----
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 1326
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ORGANISM: Homo sapiens
-09-688-188B-15
                                                                                                                                                                                                                                                                                                               Jest_Local Similarity
Autohes 90, Conserva
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294 186 343

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 VWRHFALDAAATVAAQRDTTVISHSPNTSYDTALBARIQKEEEBILMANKRCLDMBGRIK 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 ALEKAMRNKI.EGEIRRMHD------FURDI.RERI.ETANKQLAEKEYEGSED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 SNAQAKVVKLEEELKKKKOV----YVDKV----EKMQQALVQLQAACBKREQLEHRLRTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 179; Gaps
                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Bwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
TITME OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 2482;
                                                                                                                                                                                                                                                                                                                             CONTRESSORTING ADDRESS:
CAMPRESSENCE ADDRESSES:
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
CUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING BATE: 24-OCT-1994
CLASSIPICATION: ADDRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.8%; Score 226.5; DB 1;
Best Local Similarity 21.4%; Pred. No. 1.8e-06;
Matches 139; Conservative 100; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION: 339
PRIOR APPLICATION: 339
FILING DATE: 22-CCT-1993
ATTORNEY AGENT INCORMATION:
NAME: Campbell, Cathryn A.
RECISTRATION NUMBER: 91.815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9901
SEQUENCE CHARACTERISTICS:
                                                             RESULT 11
US-08-328-254-6
; Sequence 6, Application US/08328254
; Sequence 5, Application US/08328254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
308 APATPSS 314
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GENERAL INFORMATION:
TITLE OF INVENTION:
APPLICATION ARROYNOSA FOR DIAGNORMAS
TITLE OF INVENTION:
APPLICATION: ARROYNOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROYNOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROYNOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROYNOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32957
                                                                                                                                                                                                                                                                                                                                                         638 PISEGPGPSPNPPAWVRPDNEAPPKVPQRTSSIALMTSGAGGSRPAQ-----AVR 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 MIKVLOORSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMBEKRD---- 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SKLFETLVKDGEKAE------KEAKSDVDAQVGAAKASARSAKSKV-DEVRDRALG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGT--------BSNKTAAVAPISVPAPVAAATAAAITATAATITITT 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 ISHSPNTSYDTALEARIQKEEERILMANKRCLDMEGRIKTLHAQI------IEKDA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 KITGVSVKPAAKAAAKPAAKPAAKTAAKPAAKPAAKPAAKPAA---KPAAKKPAA 203
367 TEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMTEKRDDKSWKGSLGILLGGDYRAE 426
                                               485 KÖÖQQQLLÞG-DRKPLYHYGRGMNPADKPAWAREVBERTRMNKQQNSPLAKSKPGSTGPB 543
                                                                                                      427 YVPSTP--SPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAAATA 484
                                                                                                                                                      544 --PPIPQASPGPPG-PL---SQTPPMQRPVEPQEGPHKSLVAHRVPLK---PYAAPVPR 593
                                                                                                                                                                                                             485 AAITATAATITTIMVAAAPVAVAAAAAPAAAAAPSPATAAATAAATAAAVSPAAAGQIPAAASV 544
                                                                                                                                                                                                                                                                594 ---SQSLQDQPTRNLAAFP-----ASHDPDPAIPAPTA---TPSARGAVIRQNSD 637
                                                                                                                                                                                                                                                                                                                  545 ASAAAVAPSAAAAAVQVAPAAPAPVP--APALVPVPAPAAAQASAPAQTQAPTSAPAVA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DXSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQTE
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                                                                                                                                                                                                                                                                                                                                                                                                                      603 PTPAP------TPTPAVAQAEVPASPATGPGPHRLSIPSLTCNPD 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 ARPRSNSAWQIYLQRRAERGIPKP-----PGPPAQPPGP----PNASSNPD 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.9%; Score 231; DB 4; Length 316; Best Local Similarity 29.2%; Pred. No. 6.7e-08; Matches 107; Conservative 29; Mismatches 129; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
-09-252-991A-32957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 VPASPAT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .09-252-991A-32957
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542 ASVASAAAVAPSAAA-----AAAVQVAPAAPAPAPAPALVPAPAPAAAQASAPAQTQ 593
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                                                                                                                                                                                                       248 SASAAPSRAHLRPPSPBIQVADPPTPRPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-DBC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION UNDERE: 36,252
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 563-4040
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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ORGANISM: HUMAN
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APPLICANT: Federsen, Annette B
APPLICANT: Nielsen, Annette B
APPLICANT: Nielsen, Anne A
APPLICANT: Novies, Nielsen, Nielsen, Nielsen, Nielsen, Nielsen, US
CURRENT APPLICATION NUMBER: US 09/963,137
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-09-24
SEQ ID NOS: 215
SEQ ID NOS: 215
SEQ ID NOS: 215
SEQ ID NOS: 215
SEQ ID NOS: 216
SENTHARE: PALENTIN TOTAL TOT
                                                                            2255 HLCSQQSKQDSRGSPLLGPVVPGPSPIPSVTB-----KRLSSGQNKASGKRQRSSGI 2306
                                                                                                                                                                                                                                     2307 ------WENG----GG-----PTPATPESFSKKSKKAVMSGIHPAB 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2376 ATRTSP-RLAAOKLALSPLSLGKENLAES----SKPTAGGSRSOKVKVAORSPVDSGT 2428
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                                                                                                                                                                                                                                                                                                                     457 TERGTESNKTAAVAPISVPAPVAAATAAAITATAATI--TTTMVAAAPVAVAAAAPAA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 AAAPSPATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAVQVAPAAPAPVPAPA 574
341 TLHAQIIEKDA----MIKVLQQRSRKEPSKTEQLSCMRPAKSIMSISNAGSGLLSHSSTL 396
                                                                                                                                                             397 TGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQ 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 -----PSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAATAA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 KPAPAAQAVSTGSDAGAPTDSAMLTDS -- QSDAGEDGTAPGTPSDLQSDPEELBEAPAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 RPAKSLMSIS-NAGSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRARYVPST-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575 LVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPTPAVAQABVPASPATG 625
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                                                                                                                                                                                                                                                                                                                                                                                              2338 DIEGTE----FRPEGLPEVVKKGPADIPTGKTSPYILRRTTM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 184, Application US/09963137
Patent No. 6596036
GENERAL INFORMATION:
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2103 AEVKEKTELLQTLSSDVSELLKDKTHLQEKTQSLEKOSQALSLTKCELENQLAÇLNKEKE 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2163 LIVKESESLQARLSESDYEKUNVSKALEAALVEKGEPALRLSSTQEEVHQLRRGIEKURV 2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 PAMSASÁRAÁAARAÁYAGPLVWGARSLSATPAÁRÁSLÞÁRÁ--AAAÁRÁSAÁSAÁRÁVAAGR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 NLVKSSSK------REALEKAMRNKLEGEIR-----RMEDFNR---DLRB 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLETANKQ---LAEK-----EYEGSEDTRKTISQLFAKNKESQR----BKEKLEAELAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 ARSTNEDQRRHIEIRDQALSNAQAKVVKLEBELKKKQVYVDKVEXM------QQA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------VETBIQRVSEAYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 132; Gaps
                                                                                                                                                             Sequence 1, Application US/08353700
Patent No. 559919
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTUER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                          ----PRPTAWPDK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.7%; Score 225; DB 1; Length 3248; Best Local Similarity 21.4%; Pred. No. 3.2e-06; Matches 110; Conservative 106; Mismatches 167; Indels 13:
                                      594 APTSAPAVAPTPAPTPTPAVAQABVPASPATGPGPHRLSIPSLTCNPDK
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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Oy 20 AIVSRAQOMVEHISDENRNLRQELEGCYEKVARLOK	OY 274 OKVLBENVMRHFALDAATVAAORDTTVISHSPNTSYDTALEAR 317	US-09-489-039A-7502 Sequence 7502, Application US/09489039A Sequence 7502, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION: APPLICANT: Gary Breton et. al TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TILLE OF INVENTION: NUMBER: 1099-40031CS AND THERAPEUTICS TILLE REFERENCE: 2709.2004001 CURRENT PALLING DATE: 2000-01-27 PRIOR PLILING DATE: 1999-01-27 PRIOR FILLING DATE: 1999-01-29 PRIOR FILLING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 7502 LENGTH: 1079 TYPE: PRT CRGANISM: Klebsiella pneumoniae US-09-489-039A-7502	Query Match 6.7%; Score 223.5; DB 4; Length 1079; Best Local Similarity 22.3%; Pred. No. 1e-06; Matches 145; Conservative 65; Mismatches 266; Indels 175; Gaps 25; Qy 1 MPRAQPSSASYQEVPADPFAIVSRAQQWVELLSDENRALRQELEGCYEKVARLQK 55 Db 536 MPDAPPAPHLEEPAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAAPVAAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAPVAAAAAPVAAAAPVAAAAAPVAAAAAPVAAAAAA
2283 LKTOIEEMARSLKIPELDLVTLRSEKENLITKQIOEKQGQLSELDKLLSSFKSLLEEKEQA 2342 201 IJVOLQ	SULT 14 T-US95-16216-1 Sequence 1. Application PC/TUS9516216 GENERAL INFORMATION: APPLICANT: Rattner, Jerome B. TITLE OF INVENTION: TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use NUMBER OF SEQUENCES: 4 CORRESPONDENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: Dann, DOTHER OF SHILMan STREET: 1601 Market Street Suite 720 CITY: Philadelphia	CR. A PER LA PRINCIPIE DE LA P	TEMEPHONE: (215) 563-4100 TEMEPAX: (215) 563-4044 INFORMATION FOR SEG 1D NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3248 amino acids TYPE: amino acids TYPE: amino acids TYPE: not relevant TOPOLOGY: not relevant MOLECULE TYPE: protein HYPOTIETICAL: NO ANTI-SENSE: NO TT-U895-16216-1 Query Match G-7%; Score 225; DB 5; Length 3248; Best Local Similarity 21.4%; Pred. No. 3.2e-06; Matches 110; Conservative 106; Mismatches 167; Indels 132; Gaps 21;

235 71.1	292	352 765	412 808	460	520 923	577 983	
6 KVVKLBEELKKKQVYYDKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESLRIQQRQ	6 GNCOPINVSEYNAAALMELLREKEERILALEADMIKWEOKYLEENVMRHFALDAAAIT	3 VAAQRDITVISHSPNTSYDTALBARIQKEBEEILMANKRCLDMEGRIKTLHAQIIBKDAM : : : : : :	3 IKVLQQRSRKEPSKTEQLSCVRPAKSLÆSISNAGSGLLSHSSTLTGSPIMEEKRDDKSWK : :	3 GSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGS	1 TESNKTAAVAPISVPAPVAAAATAATITATAMAAAPAAAAPAAAAAPBP	atarataranspargoiparasvasaravapsararanqvapareapupurdel-vp 	8 VPAPAAQASAPAQTQAPTSAPAVAPTPAPTPTPAVAQAEVPASPATGPGP 628
176	236	293	353	413	461	521	578 984

arch completed: June 16, 2004, 19:13:23 ctime: 31.0562 secs

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June 16, 2004, 19:10:47; Search time 65.1895 Seconds (without alignments) 2917.113 Million cell updates/sec
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1 MPRAQPSSASYQPVPADPPA.....KTPIQILGQEPDAEMVEYLI 675
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1: /cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

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18: /cgn2 6/ptodata/2/pubpaa/USO08 PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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rfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 87, Appl Sequence 2, Appli Sequence 4, Appli		Sequence 36456, A Sequence 83, Appl	169	Sequence 37, Appl Sequence 149, App	Sequence 149, App Sequence 33, Appl	Sequence 3279, Ap Sequence 33686, A
SUMMARIES	US-10-204-887-87 US-10-298-417-2	US-10-094-466-52 US-10-260-715-8	US-09-864-761-36456 US-10-171-311-83	US-10-184-644-169 US-10-184-634-169	US-10-063-685-37 US-10-184-644-149	US-10-184-634-149 US-10-063-685-33	US-10-369-493-3279 US-10-029-386-33686
DB	44	151	9 1	14	14	11 14 14 14	15
% Query ore Match Length DB II	608 882	467	208	2846 2846	2846	2773	1965 980
% Query Match	4. 4. C	3.0.0 0.4.0	8 8	9.7	9.7	7.9	7.7
Score	1447	1037	278	265.5	265.5	264.5	263.5
ssult No.	1 400	ላ 4 L	700	00 O	110	12	11 44 5

HODGSON, David M.

, App	Appl	Appl	App3	Appl	Appl	Appl	Appl	App1	App1	Appl	Appl	Appl	Appl	App1	Appl	9, Ap	Appl	Appi	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
-10-363-616-4	-10-184-644-7	-10-184-634-7	-142-426-9	-10-123-155-9	-10-146-731-9	-10-140-472-9	-10-141-761-9	-142-885-9	-10-158-790-9	US-10-137-871-99	-10-140-923-9	56-9	-10-141-759-9	-10-140-805-9	9	-408-765A-	-10-146-473-5	2-426-3	-10-123-155-	-10-146-731-3	-10-140-472-	ç	-882-3	-158-790-	-10-137-871-	-923-	-756-3	-10-141-759-	-805-3	
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258	258	258	256.5	256.5	256.5	256.5																			252					
16	17	18	13	20	21	22	23	24	25	26	27	28	00	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

; Sequence 87, Application US/10204887; Publication No. US20030124569A1; GENERAL INFORMATION: ROSEN, Bruce H. RUSSO, Frank D. STOCKDREHER, Theresa K. GENERAL LINCORDATION

APPLICANT: PANZER, SCOLT R.

APPLICANT: SPIRO, Peter A.

APPLICANT: SPIRO, Peter A.

APPLICANT: SHAH, Purvi

APPLICANT: SHAH, Purvi

APPLICANT: CHALUP, Michael S.

APPLICANT: CHANG, Simon C.

APPLICANT: CHEN, Alice

APPLICANT: D'SA, Steven A.

APPLICANT: D'SA, Steven B.

APPLICANT: DANIELS, Susan E.

APPLICANT: DANIELS, Susan E.

APPLICANT: DIROUGH, Gerard B. FONG, Willy T. GREENAWALT, Lila B. HILLMAN, Jennifer L. JONES, Anissa L. DAFFO, Abel
WRIGHT, Rachel J.
YAP, Pierre B.
VJ, Jimmy Y.
BRADLEY, Diana I.
BRADLEY, Shawn R. LIU, Tommy F. ROSEBERRY, Ann M. US-10-204-887-87 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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APPLICANT: Yoshimi Takai
TITLE OF INVENTION: Exocrine gland tight junction-constituting protein JEAP family
FILE REFERENCE:
CURRENT PELICATION NUMBER: US/10/298,417
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: JP 2001-352241
PRIOR APPLICATION NUMBER: JP 2001-352241
SPRIOR PILING DATE: 2001-11-16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 10
SEQ ID NOS: 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVAAQRDITVISHSPNTSY-DTALEARIQKBEBEILMANKRCLDMEGRIKTLHAQIIBKD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          632 AATAERDTTISNHSRNGSYGESSLEAHIWPEBEEGVVQANRRCQDMEYTIRNLHAKIIEKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.8%; Score 1400; DB 14; Length 58.2%; Pred. No. 1.8e-71; tive 80; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 E-----SNKTAAVAPISVPAPVAAATAA 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.2%
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                    LENGTH: 882
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-298-417-2
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                       APPLICANT: LINCOLN, Stephen E.
TITLE PERENCE: PT-1134 PCT
CURRENT APPLICATION NUMBER: US/10/204,887
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/185,215; 60/205,232; 60/205,323; 60/205,287; 60/205,324; 60/205,324; 60/205,224; 2000-05-16; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
PERATURE:
NAWE/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030124569A1 L1:212029.1.orf2:2000FBB01
PERATURE:
NAME/KEY: unsure
LOCATION: 18, 388
OTHER INFORMATION: unknown or other
10-204-887-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 PQPPPAASPSQQLGPDAFAIVERAQQMVEILTEENRVIHQELQGYYDNADKIHKFEKELQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 EELREKQAYVEKVEKLQQALTQLQSACEKREQWERRLRTWLERBLDALATQQXHGNGQPA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 NVSEYNAAALMELLREKBERILALEADMIKWEQKYLEENVWRHFALDAAATVAAQRDTIV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 RKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMEERRDDKSWKGSLGILLG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 RVSEAYENLVKSSSKREALEKAMRNYLEGEIRRMHDFNRDLRERLFTANKQLAEKSYEGS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 EDTRKTISQ1FAKNKESQREKEKIABALATARSTNEDQRRHIEIRDQALSNAQAKVVKLE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 BELKKKOVYVDKVZKXXQQALVQLQAACEKRQLEHRLRTRLERELBSLRIQQRQSNCQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PRAQPSSASYOPVPADPFAIVSRAQOMVBILSDBNRNLRQBLBGCYEKVARLQKVBTBIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.2%; Score 1447; DB 14; Length 608; Best Local Similarity 62.1%; Pred. No. 2.4e-74; Matches 293; Conservative 79; Mismatches 84; Indels 16; Gaps
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-10-298-417-2
behavence 2, Application US/10298417
behavence 2, Application US/10298417
behavence 2, Application US/10298417
GENERAL INFORMATION:
APPLICANT: Mayuki Nishimura
APPLICANT: Wuichi Ono
APPLICANT: Koji Morimoto
APPLICANT: Koji Morimoto
APPLICANT: Yoko Inoue
APPLICANT: Toshio Imai
```

Sequence 4, Application US/10298417

Publication No. US20030124603A1

GENERAL INFORMATION

APPLICANT: Mayumi Agano

APPLICANT: Vuichi Ono

APPLICANT: Voi Morimoto

APPLICANT: Voi Morimoto

APPLICANT: Voko Inoue

APPLICANT: Voko Inoue

APPLICANT: Yoko I

```
PRIOR APPLICATION NUMBER: 60/275,5,5
PRIOR FILING DATE: 2001-03-13
PRIOR PLING DATE: 2001-03-13
PRIOR PLING DATE: 2001-10-31
PRIOR FILING DATE: 2001-10-31
PRIOR PLING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/276,000
PRIOR PLING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/276,000
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
PRIOR PLING DATE: 2011-03-20
PRIOR PLING DATE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.0%; Score 1037; DB 15; Best Local Similarity 48.4%; Pred. No. 3.8e-51; Matches 233; Conservative 75; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-094-466-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . S 454
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: AND WETHODS OF USING
TITLE OF INVENTION: THE SAME
FILE REPERBACE: 21402-290D
CURRENT APPLICATION NUMBER: 05/10/94,466
CURRENT PILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-05-02
PRIOR PLILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-03-12
PRIOR PLILING DATE: 2001-03-12
PRIOR PLILING DATE: 2001-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 VETEIQRVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 KEYEGSEDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 -----GNCQPTNVSEYNAAALÆBILREKBERILALBADMTKWEQXYLEENVMRHFALDA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATVAAQRDTTVISHSPNTSYDTALEARIQKSEBEILMANKRCLDMEGRIKTLHAQIIEK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 SWKGSLGILLGGDYRAEYVPS---TPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKT 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 PSSASYQPVPADPFAIV----SRAQQMVBILSD-----ENRNLRQBLEGCYEKVARLQK 55
                                                                                                                                                                                                                                                                                                                                                                              32.6%; Score 1090.5; DB 14; Length 772; 50.4%; Pred. No. 6.2e-54; tive 71; Mismatches 118; Indels 51;
           PRIOR APPLICATION NUMBER: JP 2001-352241
PRIOR FILING DATE: 2001-111-16
NUMBER: OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 772
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULT 4
:-10-094-466-52
Sequence 52, Application US/10094466
Publication No. US20030203363A1
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.4
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 AAVA 470
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130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 MANYRCLDWEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCWRPAKSLMSISNAG 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 SCLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPS-----TPSPVPP 437
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                                                                                                                Gaps
                                                                                                                26;
Length 467;
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Publication No. US2003009992A1
GENERAL INFORMATION:
APPLICANT: UCB: S.A.
APPLICANT: UCB: S.A.
APPLICANT: NOCKA, Karl
APPLICANT: HOUSA, Connected to the conne
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Sequence 83, Application US/10171311

PUDLICATION NO. US20030087270A1

GENERAL INFORMATION:

APPLICANT: Chen, Yan

APPLICANT: Chen, Yan

APPLICANT: Chen, Yan

APPLICANT: Amatkar, Shubhangi

APPLICANT: Amatkar, Shubhangi

APPLICANT: Garnavarapu, Manjula

APPLICANT: Garnavarapu, Manjula

APPLICANT: Garnavarapu, Manjula

APPLICANT: Garnavarapu, Manjula

APPLICANT: Hoersh, Sebastian

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THER

TITLE OF INVENTION: OF CENVICAL CANCER

TITLE OF INVENTION: UNBER: US/10/171,311

CURRENT APPLICATION NUBBER: US 60/298,159

PRICR APPLICATION NUBBER: US 60/298,159

PRICR PILING DATE: 2001-06-13

PRICR PILING DATE: 2001-06-13

PRICR PILING DATE: 2001-06-13

PRICR APPLICATION NUBBER: US 60/298,155

PRICR APPLICATION NUBBER: US 60/298,155

PRICR APPLICATION NUBBER: US 60/235,936
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: US 09/609,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PREPRESESED IN PETAL LIVER, SIGNAL = 5.5
POTHER INFORMATION: EXPRESESED IN PELVEN, SIGNAL = 5.5
POTHER INFORMATION: EXPRESESED IN PELVEN,
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Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-36456
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-09-864-761-36456

Sequence 36456 Application US/09864761

Parent No. US20020048763A1

Sequence 36456 Application US/09864761

Parent No. US20020048763A1

APPLICANT: Perm, Aparton G.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Ancho, Wensheng

TITLE OF INVENTION: HUMAN GENCHE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENCHE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL CHRENT APPLICANTON NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-07

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-13-0

PRIOR PILING DATE: 2000-10-13-0

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US CT/US01/0066

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%; Score 280.5; DB 14; Length 1259; Best Local Similarity 31.6%; Pred. No. 1.4e-07; Aatches 96; Conservative 34; Mismatches 109; Indels 65;
                    CURRENT APPLICATION NUMBER: US/10/260,715
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/325,536
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 1259
TYPE: RT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CEKREQLEHRLRTRLERELESLRIQQRQG------NCQP---TNVSEYNAAAL-- 251
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                                                                                                                                                                                                                                                                                  100 RDLRERLETANK--QLAEKEYEG-----SEDTRKTISQLFAKNK----BSQREKEKLEAE
                                                                                                                                                                                                                                                                                                                  465 KTAAVAPISVPAPVAAAATA-----AAITATAATITTTMVAAAPVAVAAAAAAA
                                                                                                                                                                                     Query Match
8.2%; Score 275; DB 14; Length 2701;
Best Local Similarity 25.1%; Pred. No. 7.3e-07;
Matches 156; Conservative 94; Mismatches 207; Indels 164; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------PATLTPVPAS-----
NUMBER OF SEQ ID NOS: 238
SOFTWARE FRACSEQ for Windows Version 4.0
SEQ ID NO 83
LENGTH: 2701
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                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
-10-171-311-83
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SULT 8
-10-184-644-169
Sequence 169, Application US/10184644
Publication No. US20030044930Al
GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sanith, Victoria
APPLICANT: Sanith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Xanith APPLICANT: Zhang, Zemin

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US-10-184-634-169

US-10-184-634-169

US-10-184-634-169

Sequence 169, Application US/10184634

Publication No. US20030068684A1

GENERAL INFORMATION:

APPLICANT: Baker,Kevin P.

APPLICANT: Desnoyers,Luc

APPLICANT: Goddard,Audrey

APPLICANT: Goddard,Audrey

APPLICANT: Gordowski,Paul J.

APPLICANT: Gordowski,Paul L.

APPLICANT: Garney,Austln L.

APPLICANT: Garney,Austln L.

APPLICANT: Smith,Victoria

APPLICANT: Smith,Victoria

APPLICANT: Aranabe,Colin K.

APPLICANT: Applicanion SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION UNUSER: US/10/184,634

CURRENT APPLICATION NUMBER: US/10/184,634
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME PILE REPERBRICE: 93430R1C227 CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT PILING DATE: 2002-06-28 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 LENGTH: 2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 TGSRDCSTQT-----BRGTBSNKTAAVAPISVPAPVAAATAA-----AITATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.9%; Score 265.5; DB 14; Length 2846;
Best Local Similarity 42.4%; Pred. No. 2.7e-06;
Matches 81; Conservative 11; Mismatches 84; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: Homo Sapien
US-10-184-644-169
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.; ORGANISM: Homo Sapien
US-10-184-634-169
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US-10-184-634-149
Sequence 149, Application US/10184634; Publication No. US2030068684A1
GENERAL INPORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian Wood, William I. ; TYPE: DNA ; ORGANISM: Homo Sapien US-10-184-634-149 TYPE: DNA ORGANISM: Homo Sapien 2772 AG 2773 624 TG 625 US-10-184-644-149 원 셤 Š 셤 ò APPLICANT: Exton.Dan L.
APPLICANT: Exton.Dan L.
APPLICANT: Exton.Dan L.
APPLICANT: Exton.Dan L.
APPLICANT: Gerricaen,Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, (hriscopher J.
APPLICANT: Grimaldi, (hriscopher J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin W.
APPLICANT: Watanabe, Col 448 TGSRDCSTOT-----BRGTESNKTAAVAPISVPAPAAATAA-----AITATAA 492 493 TITITWVAAAAPVAVAAAAAAAAAAAAAAAAAAAAAAAAGOIPAAASVASAAAVAP 552 553 SAAAAANQVAPAAAAPAPAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPA 612 553 SAAAAAVQVAPAAAAAPAPAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPA 612 Query Match
7.9%; Score 265.5; DB 14; Length 2846;
Best Local Similarity 42.4%; Pred. No. 2.7e-06;
Matches 81; Conservative 11; Mismatches 84; Indels 15; Gaps SSULT 11
S-10-184-644-149
Sequence 194, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Beker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Modrey,
APPLICANT: Goddard, Modrey,
APPLICANT: Goddard, Nodrey,
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria Sequence 37, Application US/10063685 Publication No. US20030180909A1 GENERAL INFORMATION: 2829 AAAAAAAAAA 2839 2829 AAAAAAAAA 2839 613 VACAEVPASPA 623 613 VAQAEVPASPA 623 TYPE: DNA ORGANISM: Homo Sapien:-10-063-685-37

APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: Smith, Victoria
APPLICANT: ApplicANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ROCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT FILENGE DATE: 2002-06-28
FILE REPERENCE: P3430R1C217
CURRENT FILENGE DATE: 2002-06-28
FILE REPERENCE: P3450R1C217
CURRENT FILENGE DATE: 2002-06-28
FILE REPERENCE: P3450R1C217 2594 GITICALLITICICA--IGACAAIGIAGGAAIIGCIGAAIIAAAAIGITIAGAAGGAIGAA 2651 504 VAVAAAAAAAAAABSPATAAATAAAVSPAAGQIPAAASVASAAAAAAAAAAAAAAAAA 563 449 GSRDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAA----AP APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C27
CURRENT PPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 149 449 GSRDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATAATITTHVAA----AP 564 PAAPAPVPAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPAVAQAEVPASPA Gaps Query Match
7.9%; Score 264.5; ÚB 14; Length 2773;
Best Local Similarity 43.4%; Pred. No. 3e-06;
Matches 79; Conservative 11; Mismatches 85; Indels 7; Query Match 7.9%; Score 264.5; DB 14; Length 2773; Best Local Similarity 43.4%; Pred. No. 3e-06; Matches 79; Conservative 11; Mismatches 85; Indels 7; qq

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FILE REFERENCE: 38-10(52052)B
CURRENT PEDILCATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                         TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3279
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Sequence 3279, Application US/10369493
Bublication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                              623
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     504 VAVAAAAPAAAAPSPATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVA 563
                                                                                                                 564 PAADAPVPAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPAVAQAEVPASPA
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Best Local Similarity 43.4%;
Matches 79; Conservative
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ORGANISM: Homo Sapien
-10-063-685-33
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1570 BOOSGVSQNGVPATPAKPPTAOTAQTPGAGTPGLPDLANLTDQQTRELISSNQVIMGIIK 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 -----TISQLFAK-----NKESQREKEKLEAELATARSTNEDQREHIEIRDQAL
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                                                                                                                                                                                                                                              26 QOMVEI-----LSDENRNLRQELEGCYEKVARLOKVETEIORVSEAYENLVKSSSKREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 -MBEKKD-----DKSWKGSLGILLGGD------YRAEY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 546 SAAAVAPS-----AAAAAAQVAPAAPAPVPAPALVPVPAPAAAQASA-----5
Query Match 7.9%; Score 263.5; DB 15; Length 1965; Best Local Similarity 22.9%; Pred. No. 2.3e-06; Matches 189; Conservative 110; Mismatches 280; Indels 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1798 NPFGQPGANQSPVTSQPPANPPGAAPQQQQNAQPQQP--PATNP 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PAQTQAP-TSAPAVAPTPAPTPAVAQAEVPASPATGP 626
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598 APAVAPTPA-----PTPTPAVAQABVPASPATGPGPHRLSIPSITCNPDKTDGPVF 648
                                              completed: June 16, 2004, 19:17:09
ne: 67.1895 secs
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Job time
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                                                                                                                                                         APPLICANT: Pean, Sharron G.
APPLICANT: Pean, Sharron G.
APPLICANT: Pean, David R.
APPLICANT: HIRSEL, David R.
APPLICANT: HIRSEL, David R.
APPLICANT: HUAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OFFILE OF INVENTION: HUAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OFFILE REPERBENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33686
LENGTH: 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 MRNKLEGEIRRMHDFNRDLRERLETANKQLABKEYEGSEDTRKTISQLFAKNKESQREKE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 KLEAEL-ATARSTNEDQRRHIEIRDQALSNAQAK-----VVKGEEELKGCKQVYVDKVFKM 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 QOALIVQLQAACEKREQLEHR-----LRTRLERELESIRIQQRQGNCQPTNVSEYNAAALM 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 ELLREKEERILALBADMTKWEQKYLEENVMRHFALDAA-----ATVAAQRDTTVI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 SHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTIHAQIIEKDAMIKVLQQRSRK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 AAIVPFPHEDILVASIVSLEEBDVTAAVSAPERATVPAVTVSVPEGTAAVAAVSSPEET 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 EPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMBEKRDDKSWKGSLGILLGGD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 YRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAP-----IS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 VPAPVAAAATAAAI-----TATAATITTTMVAAAPVAVA------AAAAPA---- 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656 SPAAAVPTPEEPTSPAAAVPTPEEPTSPAAA--VPTPEEPASPAAAVPTPEEPASPAAAV 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561 QV-----APAAPAQ-----VPAP----ALVPVPAPAAQASAPAQTG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 LSDENRNLRQ----ELEG----CYEKVARLQKVETBIQRVSEAYENLVKSSSKREALEKA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 LAKDNGSLSQGDCSQTEGNGEECIERVTFSFAFNHELTDVT-----SGPEVEVLYES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 APAVAAAIT----QEGMSAVAGRSPEWAALAITV---PITEE--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --AAAAPSPATAAATAAAV----SPAAAGQIPAAASVASAAAVAPS----AAAAAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 NDTKPELNVASSEGGEMERRDSDSFLNIFPEKQV-----TKAGNTEPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 7.7%; Score 258; DB 14; Length 980; Best Local Similarity 21.9%; Pred. No. 2e-06; Matches 160; Conservative 89; Mismatches 280; Indels 200; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO AL137853.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.84
OTHER INFORMATION: SWISSPROT HIT: Q02910, EVALUE 2.00e-03
:-10-029-386-33666
                                                                      Sequence 33686, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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version 5.	- 2004
GenCore	(c) 1993
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June 16, 2004, 19:09:47; Search time 27.2311 Seconds (without alignments) 2384.384 Million cell updates/sec no n

US-09-332-063-2 3347 1 MPRAQPSSASYQPVPADPFA......KTPIQILGQEPDAEMVEYLI 675

tle: rfect score: quence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 oring table:

283366 seqs, 96191526 residues arched:

283366 tal number of hits satisfying chosen parameters:

nimum DB seq length: 0 ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4						
Sult No.	Score	Query Match	Length	DB	ID	Description
r-4	300	0.0	1087		OFMSH	neurofilament trip
2	292	8.7	507	Ŋ	T44768	
m	286.5	8.6	2346	N	T13829	
4	285.5	8.5	1072	el	A37221	ofilamer
ιń	280		3534	N	T42567	ŭ
9	279	8 3	801	(3	T29018	hypothetical prote
۲	278		600	7	T29879	hypothetical prote
ω	74	8.2	1299	7	T47182	
σ	263.5	7.9	352	N	A36128	
10	57	7.7	416	7	SKKLAG	dermal gland prote
11	252	7.5	828	7	S15762	neurofilament trip
12	250.5	7.5	352	N	G82990	alginate regulator
13	249	7.4	1020	-	ОЕНИН	4
14	248.5	7.4	1039	Ŋ	\$18199	myosin heavy chain
15	245.5	7.3	2094	7	833124	tpr protein - huma
9	243.5	7.3	1334	7	T50568	probable multi-dom
12	243	7.3	473	7	S50755	hypothetical prote
82	242		217	7	829309	hypothetical prote
6	242		309	~	G83013	polyhydroxyalkanoa
20	242	7.2	915	7	836327	clathrin assembly
디	240.5	7.2	865	6	A47282	ind
22	240.5	7.2	873	8	A47283	calphotin - fruit
ຊ	238.5	7.1	581	N	T22341	cal
24	238.5	7.1	854	ď	802003	₩,
53	237	7.1	340	N	A35630	y pr
98	236.5	7.1	1132	7	C75259	probable iron-sulf
7	234	7.0	106	7	482	otei
28	234	7.0	1110	7	511	NF-180 - sea lampr
62	231.5	6.9	721	7		hypothetical prote

cell wall surface	clathrin assembly	hypothetical prote	glucan 1,4-alpha-g	cell-cycle-depende	antifreeze glycopr	hypothetical diver	slow myosin heavy	hypothetical prote	hypothetical prote	myosin heavy chain	myosin heavy chain	probable arabinoga	hypothetical prote	glycoprotein X pre	myosin heavy chain
E95206	S36326	T48814	S48478	PC4035	A38420	T38459	A59234	T00391	T24591	JX0178	A59287	\$55925	T22976	VGBEXI	807537
7	0	N	-	N	O	7	7	~	~	-	N	(1	Ń	Н	Ċ
4776	896	1952	1367	1017	822	1794	1933	1736	443	1938	1940	215	1133	797	412
6.9	6.9	6.9	8.9	6.8	6.8	8.9	6.7	6.7	6.7	6.3	6.7	9.9	9.9	9.9	9.9
233	230	229.5	227.5	226.5	226	226	225	224.5	224	223.5	223	222.5	222.5	221.5	221
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

323

354

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Tpr homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession 113829
R;Zimowska, G; Aris, J.P.; Paddy, M.R.
J. Cell Sci. 110, 927-944, 1997
A;Title: A Drosophila Tpr protein homolog is localized both in the extrachromosomal chan A;Reference mumber: Z17786; MUID:97296455; PMID:9152019
A;Accession: T13829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1497 AARLEKVRSELEEVÄNQ-----LRALKDEHEKITKECDEVKKRIEPEIDISAI 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LTROLGSQOSTKPSTS-SVA 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                           185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRCLDMEGRI----KTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCWRPAKSLMSISNA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ATAPTAATPARAARAATPATAATLATAATPATPATPATAATDATAATPARAATPATP 305
                                                                                                                                                                                                                                                        |:| |::|| ::|| ::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|
                                                                                                                                     66 тратаатратаатаатаатаатаатрагааграгаатратаатратаатаата
                                                                                                                                                                                                              ------AAITATAATITTIMVAAAPVAVAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                    527 AAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAA-PAPVPAPAPALVPVPAPAAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                186 ARAATPATAATAATAATAATAATAATAATPARAARAATPATATPATATPATAATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASAP------AQTQAPTSAPAVAPTPAPTPAV--------AQAEVPASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Achlecule type: mRNA
A;Residues: 1.-2346 <2IM>
A;Cross-references: EMBL:U91980; NID:g1923273; PID:g1923274; PIDN:AAC47506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGSEDTRKTI-----SQLFAKNKESQ---REKEKLEAELATARSTNEDQRRHI-EIRDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 ALSNAQAKVVKLEEELK-KKOVYVDKVEKMQQALVQLQAACEKREQLEHRLR----TRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 ERELESTRIQORQCNCOPTNVSEYNAAALMELLREKEERI------LALEADMTKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VPADPFAIVSRAQOMVEILSDENRNLRQELEGCYBKVA----RLQKVETEI------Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 RVSEAYE-NLVKSSSKREALEKAMRNK--LEGEIRRMHDFNRDLRERLETANKQLAEKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQKY----LEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEBEBILMAN
                                                             SPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAP--ISVPAPVAAAATA
50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2346;
Indels
91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

8.6%; Score 286.5; DB 2;
Best Local Similarity 22.5%; Pred. No. 0.00041;
Matches 157; Conservative 124; Mismatches 259;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |: |::|| :| :
K---DINQRLTRENESLHMRINQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cross-references: FlyBase: FBgn0013756
A, Map position: 2R
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6
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   623 ATGPGP 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAATP 311
86;
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                                                                    108 YIDKVROLEAHNRS----LEGERAALROQKGRAAMGELYEREVREMRGAVLRLGAARGOL 163
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Genetics:
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                                                                                                                                                                                                              164 RLEQEHLLED----IAHVRORLDBEBAROREBABABABABABABABABVELOKKAQALQ
                                                                                                                                                                                                                                                                                       172 -----NAQAKVVKLEBELK------KKQVYVDKVEKMQQALVQLQA-ACE
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Pred. No. 4.6e-05;
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Molecule type: DNA
Residues: 1-507 <CHE>
       LVKSSSKREALEKAMRNKLEGEIRRMHD---
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Qy 70 LVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQL 113 :	114 AEKEYEGSEDTRKTISQLFAKNKESQREKEKLEAEL-ATARSTNEDQRRHIEIRDQALSN ::	OY 173 AQAKVVKLEBELKKKQYYVDKVEXMQQALVQLQAACEKRE	OY 213QLEHRIRTRIERBIJSLRIOOROGNCOPTNVSBYNAALMELIREKEE 260	OY 261 RILALEADMTKWEQKYLEKNVWRHFALDAAATVAAQRDTTVISHSPNTSYDTALE 315	OY 316 ARIOXEBERILMANKRCLDME	Qy 347 IEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLT 397 ::: ::: : bb 434 VKSEEKIKVV-EKSEKETVIVEEQTEEIQVTEEVTEEEDKEAQGEEEBEAGEEGGERAATT 492	OY 398 GSPINEEKRODKSWKGBLGILLGGDYRAEYVPSTPSPPPPFFPLLSAHSKTGSRDCSTQT 457	Qy 458 ERGTESUKTAAVAPISVPAPVAAAATAAAITATAATITTTWVAAAPV-AVAAAAPAA 514	S15 AAAPSPATAAAYSPAAGQIPAASYASAAAYAPSAAAAAAVQVAPAAP			Qy 623 ATGPGPHRLSIPSLTCNPDKTDGPVFHSNTLERKTP1QILGQE 665 	equine herpesvirus 4 (strain NS80567) pesvirus 4 0567	C,Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000 C,Accession: T42567 R.A.; Berry, J.; Cullinane, A.A.; Davison, A.J. R,Telford, B.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J. J. Gen. Virol., 79, 1197-1203, 1998	A;Tills: The DNA Sequence of equine herpesyllus-*. A;Reference number: Z22173; MUD:98264497; PMID:9603335 A;Accession: T42567 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	.ED> RMBL:AF030027; NID:9260599 :: strain NS80567	C;Superfamily: varicella-zoster virus gene 22 protein Query Match Best Local Similarity 34.4%; Pred. No. 0.0012;
386 GSGLASHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPS 438 1638 EKGNISESSPYTANVKPMSGSATVQQSATVTPWRGG		499 VAAAPVAVAAAAAPAAAAABSPATAAATAAAVSPAAAGQIPAAASVASAAVAPSA 554 	555 AAAAAVQVAPAAPAPVPAPALVPVPAP-AAAQASAPACTQAPT-SA 598	599 PAVAPTPAPTPPAVAQAEVPASPATGPGPHRLSIPS 635 1842 PSIQDGGSQSQQPSTSGSSSSSSTVVSSHSRHTPS 1876		utofilament triplet H protein - rat Species: Rattus norvegicus (Norway rat) Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Dec-1999 Accession: A7721, A2549; A30796; A32757; B25649	Neurosci. 10, 3714-3726, 1990 Title: Transfected rat high-molecular-weight neurofilament (NP-H) coassembles with vim Reference number: A37221; MUID:91038277; PMID:2230956	ACCESSION: AS 721 Status: preliminary; not compared with conceptual translation Molecule type: mRNA Basidnes, 1,1072 , CMI.	Cross-references: GB:AF031879; NID:g2642597; PIDN:AAB87068.1; PID:g2642598 Robinson, P.A.; Wion, D.; Anderton, B.H. BS Lett. 209, 203-205, 1986	Title: Isolation of a CDNA for the rat heavy neurofilament polypeptide (NP-H).	Accession: A2094: mRNA MOlecule type: mRNA Residues: 230-318/472-542 <rob></rob>	Cross-references: UB:N37227 Dautigny, A.; Pham-Dinh, D.; Roussel, C.; Felix, J.M.; Nussbaum, J.L.; Jolles, P. ochem. Biophys. Res. Commun. 154, 1099-1106, 1988 Title: The large neurofilament subunit (NP-H) of the rat: cDNA cloning and in situ det Reference number: A30796; MUID:88309090; PMID:2457365	.'E',568-613,'A',615-725, 55.1; PID:G205686 ; Goldgaber, D.; Smulowit	Title: Cloning of a cDNA encoding the rat high molecular weight neurofilament peptide Reference number: A32757; MUID:89184647; PMID:2928342 Accession: A32757	Status: preliminary Molecule type: mRNA Molecule type: mRNA Residues: 559-566, "E', 568-967, "V', 969-997, "GST", 1001-1022, "E', 1024-1072 < LIE> Cross-references: GB:J04517; NID:G205679; PIDN:AAA41692.1; PID:g205680 Superfamily: neurofilament triplet H protein	Keywords: coiled coil; heterotrimer; intermediate filament; nerve; phosphoprotein Query Match Best Local Similarity 22.1%; Pred. No. 0.00019; Matches 169; Conservative 109; Miematches 326; Indels 159; Gaps 31;	10 SYQPVPADPFAIVSRAQQMVEILSDEMRNIRQBIBGCYEKVARLQKVETEIQRVSEAYEN 6

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                                             hypothetical protein P59C12.3 - Caenorhabditis elegans CiSpecies: Caenorhabditis elegans CiSpecies: Caenorhabditis elegans CiSpecies: TS-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 CiAccession: T29879
Riwu, X.; Le, T.
submitted to the EMBL Data Library, November 1995
A; Pescription: The sequence of C. elegans cosmid F59C12.
A; Accession: T29879
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C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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R;Koehrer, K.; Beyer, A.; Wewes, H.W.; Weil, B.; Wiemann, submitred to the Protein Sequence Database, March 2000
A;Reference number: Z24378
A;Accession: T47182
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A;Molecule type: mRNA
A;Residues: 1-1299 <AAA>
A;Cross_references: EMBL;AL162004
A;Experimental source: adult testis; clone DKF2p434M1616
C;Genetics:
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Introns: 22/2; 45/3; 108/1
Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
                                                                                                                                                                             2721
                                                                                                                                                                                                                                                                    2828 SKPAAAPASKPAAAPASKPAAAPAP-SKPAAPAPAPSKPAAPAPSKPAAPA--PSKP 2884
                                                                        515
                                                                                                                                                                                                                                                                                                                                                         2769 AAPAPSKPAAAPAPSKPAAPAPSKPAAPPSKPAAAPAPSKPAAPAPAPSKPAA-APAP 2827
19;
                                                                                                                                  405 KRDDKSWKGSLGILLGGDYRAEYVPSTPSP---VPPSTP---LLSAHSKTGSRDCSTQTE 458
                                                                                                                                                                                                                                                                                                                  571
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                                           404
                                                                                                                                                                                                                                                                                                                                                                                                       572 A-PALVPVPA-PAAAQA-SAPAQTQAPTSAPAVAPTP----APTPT-PAVAQAEVPASP 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STPSPVPPSTP-LLSAHSKTGSRDCSTQ-----TERGTE--SNXTAAVAPIS---V 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPIEAPATDA---ATLETAPAPAAEPAPAAEAAGYDAPSSVPEETPAPAADETPAP 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APAAAAPSPATAAATAAAVSPA-----AAGQIPAAASVA-SAAAVAPSA----AA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APAVEETPAPAPAVEETPAPAPAAEETPAPAAABYAAPVAEETPAPAPAAETPAPAO 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Molecule type: L801 «KIR»
Cross-treferences: EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1
Experimental source: strain Bristol N2; clone ZK84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pothetical protein ZK84.1 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: i5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                 459 RGTESNKTAAVAPISVPAPAAATAAAITATAATITTTMVAAAPVAVAAAAAPA---AA
                                                                                                                                                                                                                                                                                                                516 AAPSPATAAATAAAVSPAA--AGQIPAAASVAS--AAAVAPSAAAAAVQVAPAAPAPVP
  Gaps
  80;
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larity 33.7%; Pred. No. 0.00025;
Conservative 18; Mismatches 91; Indels
  26; Mismatches 111; Indels
                                             361 RKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIME---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TPTPAVAQAEVPAS-----PATGPGPHRLSIPS 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          686 AAESTPAPAPARETPASAPAAESTPAPAPAAESAPAPA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirsten, J.

Limitted to the EMBL Data Library, April 1995

Description: The sequence of C. elegans cosmid ZK84.

Reference number: Z20553

Accession: T29018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPVAAAATAAAITATAATITTTMVAAAPVAVAAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2885 AAAPAPSKPAAAPAPSKPAAAPAPSKPQMIL 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623 ATGPGPHRLSIPSLICNPDKTDGPVFHSNTL 653
  Matches 114; Conservative
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                                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------AKPAAKPAAKPAAKPAAKTAA- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GKPAAKPAA-KPAAKPAAKTAAAKPAAKP------AAKPVAKPAAKP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 PAAAAAPSPATAAATAAAVSPAAAGQIPAAASVASAAAAVAPSAAAAAVQVA-PAAPAPV 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 CLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermal gland protein APBG precursor - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Baces 30-59-1991 #sequence_revision 30-8ep-1991 #text_change 16-Jun-2000
C;Accession: S07498; A34140
R;Gmachl, M.; Berger, H.; Thalhammer, J.; Xreil, G.
R;Gmachl, M.; Berger, H.; Thalhammer, J.; Xreil, G.
A;Fitle: Dermal glands of Xenopus laevis contain a polypeptide with a highly: A;Reference number: A34140; MUID:90127399; PMID:2298293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 AKPAAKPAAKPAAKPAAKPVAAKPAAKPATAPAAKPAATPSAPAASSAASATPAAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 571 PAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPT--PAPTPT-PAVAQAEVPASPATG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AjMolecule type: mRNA
AjRolecule type: mRNA
AjRolecule type: mRNA
AjRolecule type: Land cGMA>
AjCross-references: EMBL:X51394; NID:g64547; PIDN:CNA35759.1; PID:g1334643
AjRote: the authors translated the codon TTC for residue 8 as Pro
CjSuperfamily: dermal gland protein APBG; trefoil homology
CjSuperfamily: tandem repeat
Fil-20/Domain: signal sequence (fragment) #status predicted cSIG>
Fil-1416/Product: dermal gland protein APBG #status predicted cMAT>
F;23-344/Region: alanine/glutamic acid/glycine/proline-rich repeats
F;349-339/Domain: trefoil homology cTRF>
F;349-375,359-374,369-386/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 BOLEHRLATRLERELESLRIQORQCNCQPTNVSEYNAAALMELLREKEERILALEADMTK
                                                                                                                                                                                ---VEHLEGACK------QALVDSEKLLAKLEKQRGK
                                                                                                                                                                                                                                             272 WEQKYLEENVWRHFALDAAATVAAQRDTTVISHSPNTSYDTALBARIQKEBBEILMANKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 PSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATA
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                                                                                                                                                                                                                                                                        117 PAPAPAEGEAPAPAEGEAPAPAE-GEAPAPAEGEAPAPAPAEGEAPAPAEGEAP
                                                                                                                                                                                                                                                                                                                                                                                                         --DVQESLKLAQGVGKVKEAAGKALESRKAKPATKPAAKAAAKPAVKTVAAKRA-----
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                                                                            95,
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                       Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.7%; Score 257.5; DB 1; Length ilarity 34.2%; Pred. No. 0.00088; Conservative 16; Mismatches 113; Indels
                                                                            Indels
                       ; Score 263.5; DB 2;
; Pred. No. 0.00042;
43; Mismatches 169;
                          7.9%;
                                                 Best Local Similarity 26.63
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                      16 QUISHSL-
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                          Query Match
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Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gulatory protein algp - Pseudomonas aeruginosa
Species: Pseudomonas aeruginosa
Date: 30-Nov-1990 Msequence_revision 03-Feb-1994 #text_change 15-Oct-1999
Accession: A36128; JQ0148
Deretic, V.; Konyecsni, W.M.
Bacteriol. 172, 5544-5554, 1990
Title: A procaryotic regulatory factor with a histone HI-like carboxy-terminal domain:
Reference number: A36128; MUID:91008921; PMID:1698761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A36128
Status: preliminary
Accession: A36128
Status: preliminary
Accession: A36128
Status: preliminary
Accession: A36128
Status: 1-35. <a href="https://documents.org/">documents.org/</a>
Cross-references: GB:MS7551; GB:M36050
Experimental source: isolate cystic fibrosis
Note: the authors translated the codon GCC for residue 311 as Ser
Note: L: Kitano, K:; DeVault, J.D.; Kimbara, K.; Chakrabarty, A.M.; Misra, a84, 31-38, 1989
Title: Nucleotide sequence of a regulatory region controlling alginate synthesis in F Reference number: JQ0132; MUID:90108714; PMID:2514124
Accession: JQ0148
Status: translation not shown
                                                                                                            27;
                                                                                                                                                                                                                                                                           242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 TSSSAPASAPPIPILASVGTPASVTILASASIPILASALASTSAPTPAPAPASSPAAPVI 435
                                                                                                                                                                                                                                                                                                                                144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 INNYASVVIIDDHPEVTVIEDPOSNINDDGFTEVVSKKQQ-----KRLQDERRRKK--E 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 EQVIQVWNKKNANEKGRSQISKLPPRPAKKQATGIQQAQSSASVPPLASAPLPSISASV 309
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                                                                                                                                                                                                                                                                                                                                                                                    ---MELLREKEERILALEADMIKWEQKYLEE-NVMRHFA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                         145 VDLINGSSAHHQBGVPNGTGQKNSKDSTGKKRE-----DPKPGPKKPKEKVDALSQFD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDAAATVAAQRD---TTVISHSPNTSYDTALEARIQKEBEBILMANKRCLDMEGRIKTLH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---IGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562 VAPAAPAPVPAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPTPAVAQAEVPAS 621
                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                 91 SSÓRPV-----DRONRRGINGPPKSGRNFSGPRINFRKSGPPSKSGKRGPFDDØPAGTTG
                                                                                                                                                              138 SQREKEKLEAELATA-RSTNEDQRRHIEIRDQALSNAQAKVVKLEBELKKKKQVYVDKVEK
                                                                                                                                                                                                 AQIIB----KDAMIKVLQQRSRKEPS-KTEQLSCMRPAKSLMSISNAGSGLLSHSSTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 STQTERGTESNXTAAVAPISVPAPVAAAATA-----AAITATAATITTTMVAAAPVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%; Score 274.5; DB 2; Length 1299;
ilarity 25.5%; Pred. No. 0.00065;
Conservative 83; Mismatches 191; Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------PATLTPVPAS
                                                                                                                                                                                                                                                                           197 MOQALVQLQAACEKREQLEHRLRTRLERELESLRIQQRQG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486 PAQNPLQTTSQSSKQPPPSIRLPSAQ-TPNGTD
                                                                                                                                                                                                                                                                                                                                                                                       243 VSEYNAAAL------
                                                                               Local Similarity
DKFZp434M1616.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 PASTSAPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
                                                                                                            146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344
                                                                                  Best Loca
Matches
  Note:
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repetitive

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alginate regulatory protein AlgP PAS253 [imported] - Pseudomonas aeruginosa (strain PAO] c; Species: Pseudomonas aeruginosa C; Species: Dsec-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: G82990 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bi adman, S.; Yuan, Y.; Barody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Earbig, K.; Lim, J.; Lie: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, Reference number: A2956; MUID:20437337; PMID:10984043 A, Accession: G82990 A, Status: preliminary A, Wolecule type: DNA A, Residues: 1-352 ASTO-A, COSS-references: GB:AB004937; GB:AB004091; NID:99951553; PIDN:AAG08638:1; GSPDB:GN00 A, Experimental source: strain PAO1 C, Genetics: A, Genetics: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 - VXTVAAKPAAKPAAKPAAKPAAKPAAKPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 DCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITA-TAATITTTWVAAAPVAVAAAA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280
                                                                                                                                                                                                                               RARIVPSIPSPVPPSIPLLSAHSKIGSRDCSTQIERGIESNKTAAVAPISVPAPVAAAAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATPKVISPE-----KPATPEXPTPEXAITPEKVRSPEKPTPEKVVSP-E 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 HSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 QOLSHSL-----VEHLEGACK------QALVDSEKILAKDEKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AGEKLHKARTKLQDAAKAGKTKAQAKARETIS-DLEEALDT-IKAR-QADTRTYIVGLKR
                                                                                                     364 PSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMBEKRDDKSWKGSLGILLGGDY
                                                                                                                                                                                                                                                                                                                                                                         AAAITATAATITTIMVAAAPVAVAAAAAPAAAA-----PSPATAAATAAAVSPAAAGOIP
                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PKSPVTEQAKAVQKAAAEVGKDQKARKAAEKAAKEEKAASPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaasvasaaavapsaaaaavqvapaap---apvpapalvpvpapaaaqasapaqtqapts
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                                                                                                                                                              513 ERKEBERABEBRAKSDAARBGGSKKERIBEKERGEBABRBEAEAKGKAEBAĞA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673 KPASPEKPRTPEKP--ASPEKPATPEKPRTPEKPRSPEKPSSPL 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 APAVAPTPAPTPTPAVAQAEVPASPATGPGPHRLSIPSLTCNPDKTDGPV 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Score 250.5; DB 2;
25.4%; Pred. No. 0.0014;
iive 42; Mismatches 170;
                                                                                                                                                                                                                                                                                                    567 KVBKVKSPPAKSPPKSP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
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Cross-references: EMBL:X17102
Zopf, D.; Hermans-Borgmeyer, I.; Gundelfinger, E.D.; Betz, H.
nes Dev. 1, 699-708, 1987
Title: Identification of gene products expressed in the developing chick visual system
Reference number: A27040; MUID:88112814; PMID:3123320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene and
                                                                                                                                                                                                                                                                                                                                                                     Unofilament triplet M protein - chicken
Species: Gallus gallus (chicken)
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
Accession: S15762; S08061; A27040
Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.D.
cleic Acids Res. 18, 521-529; 1990
Title: Isolation of the chicken middle-molecular weight neurofilament (NF-M) reference number: S15762; MUID:90174973; PMID:2106668
Status: preliminary
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 EKLEAELATA----RSTNEDQRRH------191RDQALSNAQAKVVK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 YRRQLQSKSIELESVRGTKESLERQLSDIEERHINNDLTTYQDTIHQLENELRGTKWEMAR 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --RELESTRIQQRQGNCQPTNVS---BYNAALMELLREKEBRILALEADMT----- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KWEOKYLEENV------MRHFALDAAATVAAQRDTTVIS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | | : | | : | | 424 PSVTIASTKIQKTKIBPPKLKVQHKFVBBIIBETKVBDEKSEMEDALSAIAEE----- 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 AMRNYLEGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKTISQLFAKNKESQREK 142
                                                  27 OMVEILSDENRNIRQELEGCYEKVARLQ----KVETEIQRVSEAYENLVKSSSKREALEK 82
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          596 TSAPAVAPTPAPTP----TPAVAQAEVPA-----SPATGPGPHRLSIPSLTCNPD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Residues: 350-546,'R',548-858 <203>
Cross-references: GB:X05558; NID:g63685; PIDN:CAA29073.1; PID:g63686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.5%; Score 252; DB 2; Length 858; Best Local Similarity 19.7%; Pred. No. 0.0032; Matches 140; Conservative 104; Mismatches 248; Indels 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-858 <ZOP>
Cross-reterences: BMBL:X17102; NID:g63688; DIDN:CAA34958.1;
Zopf. D.; Dineva, B.; Betz, H.; Gundelfinger, E.
bmitted to the EMBL Data Library, November 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Introns: 355/3; 397/2
Superfamily: cytoskeletal keratin
Xeywords: coiled coil
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Accession: S08061
                                                                                                                                            642 KTD 644
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consequently,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myosin heavy chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: 22.Nov-1993 #sequence_revision 26-May-1995 #text_change 02-Feb-2001
C;Accession: S18199
R;Stewart, A.F.R.; Camoretti-Mercado, B.; Perlman, D.; Gupta, M.; Jakovcic, S.; Zak, R.J. Mol. Byol. 33, 357-366, 1991
A;Title: Structural and phylogenetic analysis of the chicken ventricular myosin heavy A;Reference number: S18199; MUID:92130260; PMID:1774788
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                                                                                                                      574
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                                                                                                                                                                                                                                                                             559 AVQVAPAAPAPAPATVPAPALVPVPA--PAAAQASAPAQTQAPTSAPAVAPTPAPTTPAVAQA 616
                                                                                                                                                                                                                                                                                                          210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
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                                                                                                                                                                                                                                                                                                                                                                                                        391 VRQLEEKSSLISQLSRGKTSFTQQIBELRRQLBEFTKSKNAL-AHALQAARHDCDLLREQ
                                                                        SAHSKTGSRDCSTOTERGTESNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAA
                                                                                                                      515 BAKSPVKEBAKSPAEAKSPEKEBAKSPAEVKSPEKAKSPAKEBAKSPPEAKSPEKEBAKS
                                                                                                                                                                         PVAVAA---AAAPAAAAPSPATAAATAAAVSPA-AAGQIPAAASVASAAAAAA
                                                                                                                                                                                                                         575 PAEVKSPEKAKSPAKEEAKSPAEAKSPEKAKSPVKBEAKSPAEAK----SPVKBEAKSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 EKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKBYEGS-----EDTRKTISQLFAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 NKESOREKEKIEAEL---ATARSTNEDOR----RHIEIRDOALSNA-OAKVVKLEBELKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 IKELÓARIBBIBBBIBBARAARAKVEKORSDIARELBELSERLBGAGGATAAOLEMNKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 KOVYVDKVEKMOOALVOLOAAC-----EKREQLEH--RIRTRERELESIR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 MELLREKEERILALEADMIKWEQ-----KYLEENVWRHFALDAAAIVAAQRDITVISHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 P-----ALEARIOKEBEBILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. Cross-references: EMBL:XS9552; NID:g62995; PIDN:CAA42130.1; PID:g62996 A; Cross-references: EMBL:XS9552; NID:g62995; PIDN:CAA42130.1; PID:g62996 A; Note: in the authors' translation 45-Lys is shown after residue 40, and, C; Superfamily: myosin heavy chain; myosin motor domain homology C; Keywords: ATP; nucleotide binding; P-loop P; 402-409/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VSRAQQMVBILSDENRNLRQBLBGCYBKVARLQKVBTBI-QRVSBAYBNLVKSSSKREAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ISKLIKEKKSLOEAHOQVLDDLQAEEDKVNRLSKAKVKLEOQVDDLBGSLEQEKKVRMDL
                                                                                                                                                                                                                                                                                                                                                                                617 -EVPASP----ATGPGPHRLSIPSLTCNPDKTDGPV-FHSNTLER-KTPIQILGQEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch
11 Similarity 23.4%; Pred. No. 0.0055;
124; Conservative 77; Mismatches 175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 IQQRQGNCQPTNVSEYNAAAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Status: preliminary
A Molecule type: mRNA
A, Residues: 1-1039 <STE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-1020/Domain: carboxyl-terminal <CTD>
2-826/Region: 14-residue repeats
3,511,518,526,532,540,546,552,560,566,574,580,586,594,600,606,614,620,628,634,640,64
2,768/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                          acies: Homo sapiens (man)
2-esies: Homo sapiens (man)
2-esion: 30-dun-1991 #text_change 16-Jun-2000
2-esion: 30-dun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
2-esion: S00979; Skuntz, S.F.; Carden, M.J.; Lazzarini, R.A.
3-7, 1947-1955, 1988
3-1-fie The structure and organization of the human heavy neurofilament subunit (NP-H)
2-ession: S00979; MUID:88328981; PMID:3138108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 perfamily: neurofilament triplet H protein words coile dela coll, heterotrimer; intermediate filament; nerve; phosphoprotein 100/Domain: amino-terminal (NTD) 1-410/Domain: amino-terminal eNTD> 1-410/Domain: rod #status predicted <ROD>
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                                281 AKPAAKPAAKPAAKPAAKPAAKPAATKPATAPAATKPATPSAPASSAASATPA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||| || : : : : || : : EGCMVAVATSRSEKEQLQALNDRFAGYIDKVRQLEAHNRS----LEGEAAALRQQQAGRS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LSNAQAXVVKLE 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : : | | : : | | : : : | | AB-TRDALKCDVTSALRAQLEGHAVQSTLQSBEWFRVRLDRLSBARKVNTDAMRSAQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNVSEYNAAALMELLREKEERILALEA-----DMTKWEQKYLEENVWRHFALDAAATVAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BEITEYR------ROLOARITELEALKSTKOSLERORSELED---RHOADIASYORAI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 SGLLSHSSTLTGSPIMEERRDDKSWKGSLGILLGGDYR----AEYVPSTPSPVPPSTPLL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPVPAPALVPVPAPAAQASAPAQTQAPTSAPAVAPT--PAPTPT-PAVAQAEVPASPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FURDLRE-----RLETANKOLAEKEYEGSEDTRKTISQLFAKNKESQREKEKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sidues: 1-1020 cLEE>
sss-references: EMBL:X15306; NID:g35028; PIDN:CAA33366.1; PID:g1841430
ee: it is uncertain whether Met-1 or Met-2 is the initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGCYBKVARLOKVETEIQRVSEAYENLVKSSSKREALBKAMRNKLEGEIRRMHD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 7.4%; Score 249; DB 1; Length 1020; Similarity 20.9%; Pred. No. 0.0051; Conservative 121; Mismatches 299; Indels 148;
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                                                                                                                                                                                                                                                                                                        ilament protein, 112K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sss-references: GDB:120225; OMIM:162230
position: 22q12.1-22q13.1
:rons: 295/1; 361/3; 403/2
                                                                                                                                                                                                                                                                               ofilament triplet H protein - human
                                                                                                                                                                                                                                                                                                          ernate names: neurof
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366 KTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDKS 410 : : : :	ර් සි	228 SIRIQ
124 124 protein - human lternate names: kinase-related transforming protein (tpr-met); protein with promoter pecies: Homo sapiens (man) ate: 22-Nov-1993 #sequence revision 26-May-1995 #text_change 11-Jan-2002 cession: 533124; 523740; 500928; G01185	60 64 64 65	258 XEERILALEADMTKWEQKYLEENVWRHFALDAAATVAAQRD-TTVISHSFNTS 309
itchell, P.J.; Cooper, C.S. ogene 7, 2329-2331, 1992 itle: The human tpr gene a protein of 2094 amino acids that has extensive coi eference number: S33124, MUID:93064711; PMID:1437155 ccession: S33124 cause: perliminary; nucleic acid sequence not shown; translation not shown	8 6 8 6	355 VLQQRSRKEPSKTEQLSCARPAKSLASISNAGSGLLSHSSTLTGSPIMEEKRDD 408 1624 HLEQRDEPQEPSINKVPEQQRQI
esidues: 1-2094 <mit> coss-references: EMBL:X66397; NID:g633225 toe: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 itchell, P.J.; Cooper, C.S. ogene 7, 383-388, 1992 itle: Nucleotide sequence analysis of human tpr cDNA clones. eference number: S23740; MUID:92195670; PMID:1549355</mit>	3 6 6 6 6	VADISVPAPVAAAATADAITATAATITTTWVAAAPVAVAAAAABAAAABSPA-TAAATA
causes: preliminary cleaule type: mRNA cleaule type: mRNE.x63105; NID:g37257; PIDN:CAA44819.1; PID:g37258 ing, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J. cygene 2, 617-619, 1988 itle: Tyr homologues activate met and raf. cleaule type homologues activate met and raf. cleaule type homologues activate met and raf.	6 6 6 6	ARACTCAPTSAPAVAPTPAPTPAVAQAEVPASPATGPGPHR
coession; SUG92: MRNA saidues: 1-31,'R',33-142 <kin> ross-references: EMBL:Y00672; NID:g37255; PIDN:CAA66681.1; FID:g37256 reco, A. itted to the EMBL Data Library, December 1995</kin>	Search c Job time	cch completed: June 16, 2004, 19:15:39 time : 31.2311 secs
iference number: H00592 :cession: G01185 :atus: translated from GB/EXEL/DDBJ :lecule type: DNA :sidues: 144-228 <gre> :oss-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798 :ne: GDB:TPR :oss-references: GDB:128821; OMIM:189940 :p position: 1q25-1q25 :trons: 177/3</gre>		
ery Match st Local Similarity 20.3%; Score 245.5; DB 2; Length 2094; st Local Similarity 20.3%; Pred. No. 0.016; tches 153; Conservative 127; Mismatches 274; Indels 201; Gaps 31; 24 RAQOWYBILSDENRALRQELEGCYEKYARLQKVETEIGRVSEAYENLVKSSSK 76		

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	protein - protein search, using sw model	31:31:01 (FOO) (FOO)	:le: US-09-332-063-2 :fect score: 3347 Juence: 1 MPRAQPSSASYQPVPADPFAKTPIQILGQEPDAEMVEYLI 675	oring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	arched: 141681 segs, 52070155 residues	:al number of hits satisfying chosen parameters: 141681	nimum DB seq length: 0 cimum DB seq length: 2000000000	st-processing: Minimum Match 0% Maximum Match 100% Listing fixst 45 summaries	:abase : SwissProt_42:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		sult Query No. Score Match Length DB ID Description	9.0 1087 1 NFH MOUSE 219246 mus mus 8.7 518 1 TPM ⁴ DROME P49455 drosopl	257.5 7.7 439 1 XP2 XENLA P17437	250.5 7.5 352 1 ALGP PSEAR P15276 pseudor	246 7.3 1026 1 NFH HUMAN 245.5 7.3 2349 1 TPR_HUMAN P12270 homo	7.2 1102 1 MYSC CHICK 7.2 915 1 A180 RAT	241.5 7.2 810 1 NFM BOVIN 077788 bos t	240.5 7.2 865 1 PROME Q02910	239 7.1 790 1 BEA1 MOUSE Q8b166 234 7.0 901 1 A180 MOUSE 061548	231.5 6.9 721 1 YK82 MYCTU Q10690 mycc 230.5 6.9 1217 1 ITNI RAT O9wve9 ratt	229.5 6.9 1935 1 MYSS_CYPCA Q90339 229 6.8 802 1 ENAH_MOUSE Q03173	227.5 6.8 1367 1 AMYH YEAST P08640 226.5 6.8 3210 1 CENP HUMAN P49454	226 6.8 790 1 ANP NOTCO P24850 226 6.8 1794 1 YDC SCHPO Q10177	223.5 6.7 907 1 A180_HUMAN 223.5 6.7 1938 1 MYSS_CHICK	223 6.7 622 1 3BP1_HUMAN Q9y31:	221 6.6 1959 1 MYH9 CHICK P14100	218 6.5 1721 1 TINI HUMAN Q1550.	31 217.5 6.5 501 1 MYSU KABIT Q93103 OLYCOLAGUS 32 217.5 6.5 1976 1 MYHA_RAT Q9jltO rattus norv 33 217 6.5 1938 1 MYS_AEQIR P24733 aequipecten

Q27991 bos taurus	P35580 homo sapien	O68032 rhodobacter	Q9bv73 homo sapien	Q9vjeS drosophila	Q9vdv3 drosophila	P12883 homo sapien	P12847 rattus norv	O08638 mus musculu	P79293 sus scrofa	P02567 caenorhabdi	Q9y618 h nuclear r
MYHA BOVIN	MYHA HUMAN	SBCC RHOCA	CEP2 HUMAN	C190 DROME	NUP1_DROME	MYH7 HUMAN	MYH3 RAT	MYHB MOUSE	MYH7 PIG	MYSD_CAERL	NCR2_HUMAN
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216.5	77	214	214	C	213	213	213		213	21.	213

ALIGNMENTS

WITH MOUSE STANDARD; PRT; 1087 AA. P19246; Q61959; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 21, Last sequence update) 01-NOV-1990 (Rel. 22, Last sequence update) 10-CCT-2003 (Rel. 22, Last sequence update) 10-CCT-2003 (Rel. 24, Last monotation update) 10-CCT-2003 (Rel. 25, Last monotation update) 10-CCT-2003 (Rel. 26, Last sequence update) 10-CCT-2003 (Rel. 27, Last sequence update) 10-CCT-2003 (Rel. 27, Last sequence in (200 kDa neurofilament protein) NEPH OR NEH. WARE MOUSEOURLE (NOUSE). NEBLARAZOA; Mercaca; Chordata; Cramiata; Vertebrata; Euteleostomi; NCBL TAXID=10090; 10. SEQUENCE FROM N.A. WARDLINE=89121513; PubMed=3220257; NGBLINE=89121513; PubMed=3220257; NGBLINE=89121513; PubMed=3145094; SEQUENCE FROM N.A. SEQUENCE FROM N.A.	Garden M.J.; Submitted (MRR-1994) to the EMBL/GenBank/DDBJ databases. Submitted (MRR-1994) to the EMBL/GenBank/DDBJ databases. Submitted (MRR-1994) to the BMBL/GenBank three intermediate filament proteins: L, M, and H which are involved in the maintenance of neuronal caliber. NP-H has an important function in mature axons that is not subserved by the two smaller NF proteins. -I- PTM: There are a number of repeats of the tripeptide K.S-P, NFH is phosphorylated on a muber of the serines in this motif. It is thought that phosphorylation of NFH results in the formation of interfilament cross bridges that are important in the maintenance of axonal calibber. -I- PTM: Phosphorylation being altered developmentally and ochnoident with a change in the neurofilament function. -I- SIMILARITY: Belongs to the intermediate filament family. -I- CAUTION: Ref.2 sequence differs from that shown in positions 534 -I- CAUTION: Ref.2 sequence differs from that shown in positions 534 -I- CAUTION: Ref.2 sequence differs from that shown in positions 534 -I- CAUTION: Ref.2 sequence differs from that shown in positions 534 -I- CAUTION: Ref.2 sequence differs from that shown in positions 534 -I- CAUTION: Ref.2 sequence differs from that shown in positions 534 -I- CAUTION: Ref.2 sequence differs from that shown in positions 534 -I- CAUTION: Ref.2 sequence differs from that shown in positions on its between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial
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648 SEAKSPAEAKSPAEAKSPAEAKSPAEVKSPGEAKSPAEPKSPAEAKSPAEAKSP 707
                                                                                                                                                                                                                                                                                                                                                                  108 AEVKSPGEAKSPAAVKSPAEAKSPAAVKSPGEAKSPGEAKSPAEAKSPAEAKSPIEVKSP 767
                                  410 SWKGSLG--ILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTA 467
                                                                                                                                                                                                                                                                                                                                            -----QAEVPA---SPATGPGPHRLSIPSLTCNPDKTDGPVFHSNTLERKTPIQILGQ 664
---VTEGVTEB--EDK 471
                                                                     472 EAQGQEGEEAEEGEEKBEELAAATS--PPAEEAASPEKETKSRVKBEAKSPGEAKSPGE
                                                                                                                                                                                                               566 APAPVPAPALVPVPAPAAAQASAPAQTQAPTSA-----PAVAPTPAPTPAVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=34; Synonym, sequence=Normannia, Name=34; Synonyms=9B; Isold=P49455-2; Sequence=VSP 006623, VSP 006624, VSP 006625; TISSUE SPECIFICITY: Both isoforms are only expressed in indirect flight muscles.
                                                                                                            468 avapisvpapaaaaraaait-ataatittitmvaaaqaaaaaaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Drosophila melanogaster tropomyosin II gene produces multiple proteins by use of alternative tissue-specific promoters and alternative splicing.";
Mol. Cell. Biol. 8:3591-3602(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPM4 DRONE STANDARD; PRT; 518 AA.

P49455; P49456; Q24425; Q24426;

T 01-FEB-1996 (Rel. 3), Latt sequence update)

T 01-FEB-1996 (Rel. 3), Latt sequence update)

T 10-OCT-2003 (Rel. 42, Last amnotation update)

T 10-OCT-2003 (Rel. 42, Last amnotation update)

T TOPOMYOSSIN 1, isoforms 33/34 (Tropomyosin II).

S Drosophila melanogaster (Fruit fly).

S Drasophila melanogaster (Fruit fly).

C Bukaryota; Methropoda; Exapoda; Insecta; Pterygota; Neoptera; Bndopterygota; Diptera; Brachycera; Muscomorpha;

K NCEL TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Karlik C.C., Fyrberg E.A.;
"Two Drosophila melanogaster tropomyosin genes: structural and functional aspects.";
Mol. Cell. Biol. 6:1965-1973 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=5; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Muscle; Synonyms=9D;
IsoCd=p06794-1; Sequence=External;
Name=Non-muscle; Synonyms=Cytoskeletal;
IsoCd=P06754-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=33; Synonyms=9C;
IsoId=P49455-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 33 AND 34).
TISSUE=Embryo, and Pupae;
MEDLINE=89127197; PubMed=2851721;
Hanke P.D., Storti R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 33 AND 34).
STRAIN-Oregon-R; TISSUE-Pupae;
MEDLINE-87064486; PubMed=3097506;
440 KVV-EKSEKETVIVEGQTEEIR-
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      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 AEKEYEGSEDTRKTISQLFAKKKESQREKEKLEAELATARSTWEDQRRHIEIRDQALS-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NAQAKVVKLEBELK------KKQVYVDKVEKMQQA£VQLQA-ACE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 SSLÓSEEWFRVRLDRLSEAAKVNTDAMRSAQBEITBYR------RQLQARTTELEALK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DMIKWEQKYLBENVMRHFALDAAATVAAQRDT --TVISHSPNTSYDTALBARIQKBE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 STKESLERORSELED---RH----QADIASYQDAIQQIDSELRNIKWEMAAQLR---E 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GRIKTLHAQI-IEKDAMI 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVSSVSASPSRFRGAASS-----TDSLDTLSNGPEGCVVAAVAARSEKEQLQALNDRFAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 SYQPVPADPFAIVSRAQQMVBILSDENRNLAQELEGCYEKVARLQKVETBIQRVSEAYEN 69
                                                                                                                                                                                                                                                                                                           ROD.
TAIL.
GLU-RICH (ACIDIC).
50 X G AA TANDEM REPRATS OF K-S-P-A-B-A.
GLU/LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 9.0%; Score 300; DB 1; Length 1087; Best Local Similarity 21.6%; Pred. No. 5.1e-05; Matches 169; Conservative 121; Mismatches 301; Indels 190; Gaps
                                                                                                                                                                                                                                                                          coil; Neurone; Phosphorylation; Repeat
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A -> AR (IN REF. 2 AND 3).

S -> T (IN REF. 2 AND 3).

L -> G (IN REF. 2 AND 3).

P -> PREAKSP (IN REF. 3).

MISSING (IN REF. 3).

G -> A (IN REF. 2).

T -> N (IN REF. 2 AND 3).

T -> N (IN REF. 2 AND 3).
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-> M (IN REF. 2 AND 3).
-> N (IN REF. 2 AND 3).
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COIL 1B.
LINKER 12.
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LINKER 2.
                                                       EMBL; M24496; AAA39813.1; --
EMBL; M24349; AAA39813.1; JOINED.
EMBL; M24494; AAA39813.1; JOINED.
EMBL; M24495; AAA39813.1; JOINED.
EMBL; M35131; AAA39813.1; JOINED.
EMBL; M35131; AAA39809.1; ALT_FRAME.
EMBL; J31022; CAA83229.1; --
PIR; JT0368; QFRH.
MGD; MGI:97309; Nefh.
InterPro; IPR001664; IF.
PROSTIT; PS00226; IF.
Intermediate filament; Coiled coll; Ner
DOMAIN 189 408 ROD.
DOMAIN 409 1087 TAIL.
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127 108 187 161

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461 388 521 469

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289 WNPRNPKPPTPKLPTPTPEBLAAMEBARAAABAAAABAAAAAGGAGAGGADGAPAAP 348
                                                                                                                                                                                                                                                                                       162 --YDEVARYLAMVEADLERAEERAEQGENKI-VELEEELRVVGNNLKSLEVSEEKAN-QR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 YVKNYEPPPGSEPEPVPAA-------BGEAAPAAGAAPPA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522 TARATARAVSPARAGQIPRARSVASARAVAPSARARAVQVAPARPAPAPALVPVPAP 581
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                                                                                                                                                       128 ISQLFAKNYESQREKEKLEABLATARSTNEDORRHIBIRDQALSNAQAKVVKLEBELKKK
                                                                                                                                                                              188 QVYVDKVEKMQQALVQLQAACEKREQLEHRLRTRLERE-----LESLRIQQRQGNCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 -- ORSRKEPS-----KTEQLSCHRPAKSLMSISNAGSGLLSHSSTLT-----GSPIM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 EGAA-----PPAEGAVPPADGAAPPAEGAAPAAEGAAPPADGAAP---PAEA----AA
68 ENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKT
                                                                                                        64 --LILVICKLERKNKALON-ABSEVAAL---NRRI-----QLLEEDLERSEERLGS
                                                                                                                                                                                                                                                                                                                                 241 TNVSEYNAAALMELLREKEBRILALBADMTKWEQKYLBENVWRHFALDAAATVAAQRDTT
                                                                                                                                                                                                                                                                                                                                                                                                                     301 VISHSPNTSYDTALEARIQKBEBEILMANKR-CLDMEGRIKTLHAQIIBKDAMIKVLQ--
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                                                                        exhibits a prominent seven-residues periodicity.

-!- SIMILARITY: Belongs to the tropomyosin family.

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EAAAIAEKARAEELAALGEEAGAEAGGGAPAEGAAPGEPG
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  DEVELOPMENTAL STAGE: Both isoforms are expressed during pupal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 292.5; DB 1; Length 518;
ilarity 24.1%; Pred. No. 4.6e-05;
Conservative 76; Mismatches 246; Indels 169; Gaps
                       adult stages.

DOMAIN: The molecule is in a coiled coil structure. The sequence exhibits a prominent seven-residues periodicity.

SIMILARITY: Belongs to the tropomyosin family.
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DLIVEKGRYCMIGDSLDBAFVDLIKGLEPFWNPRN -
IKBIBHYALVGDQLDWIFVENWGMPPFYNERY (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoform 34).
/FTId=VSP_006625.
LGSATAKLS -> SASAIQLAA (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 LGSATAKLS<sup>-</sup>-> SASAIQLAA (IN REF. 119 A -> S (IN REF. 2).
183 A -> ANVEADLERAERA (IN REF. 2).
194 V -> L (IN REF. 2).
503 P -> A (IN REF. 2).
54558 WW, 153D0872C29DB6EA CRC64;
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PRIMTS; PROD194; TROPOMYOSIN; 1.
PROSITE; PROD126; TROPOMYOSIN; 1.
Muscle protein; Cytoskeleton; Actin-binding; Coiled coil;
Alternative splicing; Multigene family.

14 267 COILED COIL
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GO; GO:0045451; P:pole plasm oskar mRNA localization; IMP
InterPro; IPR000533; Tropomyosin.
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EMBL; 100356; AAA28968.1; JOINED.
EMBL; 100359; AAA28968.1; JOINED.
EMBL; 100359; AAA28968.1; JOINED.
EMBL; 100359; AAAA28968.1; JOINED.
EMBL; 100360; AAA28968.1; JOINED.
EMBL; 100362; AAA28968.1; JOINED.
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1; JOINED.
1; JOINED.
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AAA28968.1; JOINED.
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518 AA;
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M12840;
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M12840;
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Best Local Sim
Matches 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
EMBL;
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SECURINCE OF 1-25 AND 344-439 FROM N.A. (ISOFORM 2).
MEDLINE=92332564; PubMed=1629230;
Hauser F., Roeben C., Hoffmann W.;
"xP2, a new member of the P-domain peptide family of potential growth factors, is synthesized in Xenopus laevis skin.";
J. Biol. Chem. 267:14451-14455 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repetitive amino acid sequence.";
FEBS Lett. 260:145-148(1990).
-!- FUNCTION: May act as a growth factor in the germinal layer of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-2012/1399; PubMed-2298293;
Gmachl M., Berger H., Thalhammer J., Kreil G.;
"Dermal glands of Xenopus laevis contain a polypeptide with a highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                      XP2 XENLA STANDARD; PRT; 439 AA.
P1737; 008944;
01-AUG-1990 (Rel. 15, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Skin secretory protein xP2 precursor (APBC protein).
Skin secretory forein aleawed frog).
Bukaryota; Metaca, Chordata; Craniata; Vertebrata; Buteleostc Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
628
                                                                                                          516
582 AAAQASAPAQTQAPTSAPAVAPTPAPTPAVAQAEVPASPATGPGP
                                                                                                          470 APADAAAPAABAPABAPABATAABAPABAAAPABABGBAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 3-439 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissum=skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCURATE REPORT OF THE PROPERTY OF THE PROPERT
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26; 67

12 OPVPADPPAIVSRAQOMVBILSDENRNLRQELEGCYBKVARLQK----VETBIQRVSBAY

Similarity

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:||
358 RTD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein.
INIT MET
DOMAIN
                                                                                                                                               GHIGA
                                                                                                   RESULT 4
NFM_CHICK
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 PSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 PAPAPAEGEAPAPAPGGEAPAPABS-GEAPAPAEGEAPAPAFGEAPAPAEGEAP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 APAPAPAEGEAPAPAPAEGEAPAPAEGEAPAPAPAFGEAPAPAPAFAPAPAFGEAPAPAEGEAP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 APAPAEGEAPAPAPAGGAPSPAEGGAPAAAPAEGGAPAPAPAPAPAPAPAPVEVGPKTEDCKGDPFK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKIN SECETORY PROTEIN XP2.
PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
33 X REPEATS OF G-[GB]-[AP] (2,4)-A-E.
P-TYPE 1.
P-TYPE 2.
BY SIMILARITY.
                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: SKID.
-!- SIMILARITY: Concains 2 P-type (trefoil) domains.
-!- CAUTION: Ref.2 sequence differs from that shown from position 392
-!- Onward and is shorter (418 AA) due to a frameshift.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 ATITITIMVAAAPVAV---AAAAAPAAAPSPATAAATAAAVSPA-AAGQIPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 APAPAEGEAPAPAPGEAPAPAPARGEAPAPAPAPAPAPAGEAPAPAPAEGEAPAPAPAEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 -- AASVASAAAVAPSAAAAAAVQVAPA---APAPVPAPALVPVPAPAAQASAPAQTQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596 TSAPAVAPTPAPTP----TPAVAQAEVPA-----SPATGPGPHRLSIPSLTCNPD---
epidermis. May also be involved in growth of regenerating glands and in protection of the skin from the external environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, M90095; AAA50001.1; -.
EMBL, X51394; CAA55759.1; ALT_FRAME.
PIR, A37331; A37331.
PIR, A37331; A37331.
PIR, B00495; IPS2.
InterPro, IPR00519; P. trefoil.
Ffam, PP04068; trefoil; 2.
PRINTS, PR0680; PTREFOIL.
SMART; SM0018; PD.
PROSITE, PS00025; P_TREFOIL.
PROSITE, PS00025; P_TREFOIL.
SMART; Carboxylic acid.
Prolidone carboxylic acid.
Pytrolidone carboxylic acid.
Pytrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38C4A4B57CBAB778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIId=VSP 004652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 257.5; DB 1;
34.2%; Pred. No. 0.00088;
tive 16; Mismatches 113;
                                                                                              Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=APEG;
IsoId=P17437-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> S (IN REF. 2).
                                                                                                                                                                    Name=2; Synonyms-XP2;
IsoId=P17437-2; Sequence=VSP_004652;
TISSUE SPECIFICITY: Skin.
                       and in protection of the skin f
SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.24
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642 KTD 644
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DISULFID
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CONFLICT
SEQUENCE
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MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurofilament cDNA.";

Genes Dev. 1:699-708(1987).

-!- FUNCTION: Neurofilaments usually contain three intermediate
-!- FUNCTION: Neurofilaments usually contain three intermediate
-!- FUNCTION: Neurofilaments usually contain three intermediate
-!- PTM: There are a number of repeats of the tripeptide K-S-P, NFM is
phosphorylated on a number of the serines in this motif. It is
thought that phosphorylation of NFM results in the formation of
interfilament cross bridges that are important in the maintenance
of axonal caliber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: Phosphorylation seems to play a major role in the functioning of the larger neurofilament polypeptides (NF-M and NP-H), the levels of phosphorylation being altered developmentally and coincident with a change in the neurofilament function.
                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINB=88112814; PubMed=3123320;
20pf D., Hermans-Borgmeyer T., Gundelfinger E.D., Betz H.;
"Identification of gene products expressed in the developing chick
visual system: characterization of a middle-colecular-weight
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=90174973; PubMed=2106668;
Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
Isolation of the chicken middle-molecular weight neurofilament (NF-W) gene and characterization of its promoter.";
Nucleic Acids Res. 18:521-529(1990).
                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
115-WAR-2004 (Rel. 43, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NP-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
857 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIL.
COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X17102; CAA34958.1; -.
EMBL; X05558; CAA29073.1; -.
PIR; S15762; S15762.
InterPro; IPR001664; IF.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEam; PP00038; filament; 1.
Pfam; PP04732; filament head; 1.
PRINTS; PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 259-857 FROM N.A
  STANDARD;
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406
857
130
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 DYLKTDLTTALKEIRAQLECQSDHNMHQAEEWFKCRYAKLTEAAEQNKEAIRSAKEEIAE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 LEBELKKKQVYVDKVEKMQQALVQLQAACEKR------EQLEHRLR-TRLE--- 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 YRRQLQSKSIBLBSVRGTKESLBRQLSDIEBRHNNDLTTYQDTIHQLBNELRGTKWEMAR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 HLREYQDL-----LNVXMALDIEIAAYRKLLEGEETRFSAFSGSITGPIFTHRQ 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------KWEOKYLBENV-----MRHFALDAATVAAQRDTTVIS 303
                                                                                                                                                                                                                                                                                                        27 OMVEILSDENRILRQELEGCYEKVARLQ----KVETEIQRVSEAYENLVKSSSKRBALEK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 AAASVASAAAVAPSAAAAAVQVAPAAP--APVPAPALVPVPAPAAAQASAPAQTQAPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RELESLRIQQRQGNCQPTNVS---BYNAAALMELLREKBERILALEADMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 PSVTIASTKIOKTKIEPPKLKVOHKFVEEIIEETKVEDEKSEMEDALSAIAEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 HSPNTSYDTALEARIOKEEBEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 PSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMREKRDDKSWKGSLGILLGGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 RAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 AAAITATAATITTTWVAAAPVAVAAAAPAAAA----PSPATAAATAAVSPAAAGOIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 ATPKVTSPE------KPATPEKPPTPEKAITPEKVRSPEKPTTPEKVVSP-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 BEKEÉEBBABEEBAAKSDAABBGGSKKBEIBEKEBGBBAEBBBABAKGKAEBAGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 -------PKSPVTEQAKAVQKAAAEVGKDQKAEKAAKEEKAASPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 APAVAPTPAPTPTPAVAQAEVPASPATGPGPHRLSIPSLTCNPDKTDGPV 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                            DB 1; Length 857;
                                                                                                                                                                                                                          Mery Match 7.5%; Score 252; DB 1; Length 85' set Local Similarity 19.7%; Pred. No. 0.0028; Atches 140; Conservative 104; Mismatches 248; Indels
                                                                                                                                                              G -> R (IN REF. 2).
4E2E0FC6AC64778B CRC64;
                                                                                                   COIL 2B.
O-LINKED (GLCNAC)
O-LINKED (GLCNAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              566 KVEKVKSPPAKSPPKSP------
  LINKER 1.
COIL 1B.
LINKER 12.
                                                          COIL 2A.
LINKER 2.
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E
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  143
245
259
259
261
261
406
426
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  131
144
1244
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286
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46
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546
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                                                                                                                         CARBOHYD
                                                                                                                                          CARBOHYD
                                                                                                                                                                                   SEQUENCE
DOMAIN
DOMAIN
DOMAIN
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DOMAIN
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TOTATE STANDARD; PRT; 352 AA.

PREADE PSEADE STANDARD; PRT; 352 AA.

P15276, O9HTU1; Created)

16-OCT-2001 (Rel. 10, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

17-ATABLE CONT-2001 (Rel. 40, Last annotation update)

18-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen.";
Nature 466:595-964 (2000).

-i- FUNCTION: THE PERMOTER FOR A CRITICAL ALGINATE BIOSYNTHETIC
GENE, ALGD, ENCODING GDP-MANNOSE DEHYDROGENASE, IS ACTIVATED ONLY
UNDER CONDITIONS REMINISCENT OF THE CYSTIC FIRENOSIS LING (I.E.,
UNDER ONDITIONS REMINISCENT OF THE CYSTIC FIRENOSIS LING (I.E.,
UNDER HIGH OSMOLARITY), AND AT LEAST TWO REGILATORY GENES, ALGP
AND ALGO, HAVE BEEN IMPLICATED IN THIS ACTIVATION PROCESS:
--- DOMAIN: THE CARROXY-TERMINAL BINDS TO DNA. IT IS UNKNOWN WHETHER
BINDING IS SPECIFIC OR NOW-SPECIFIC.
--- SIMILARITY: TO EUKARYOTIC HISTONES HI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC 15692 / PAO1;
MEDELINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deretic V., Konyecsni W.M.;
"A procaryotic regulatory factor with a histone H1-like
carboxy-terminal domain: clonal variation of repeats within algP, a
gene involved in regulation of mucoidy in Pseudomonas aeruginosa.";
J. Bacteriol. 172:5544-5554(1990).
                                                                                                                                                                                 Kato J., Chu L., Kitano K., Devault J.D., Kimbara K., Chu L., Misra T.K.;
"Mucleotide sequence of a requiatory region controlling alginate synthesis in Pseudomonas aeruginosa: characterization of the algR2
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                      Pseudomonas aeruginosa.
Bacteria, Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Beeudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                  regulates
                                                                                                                                                                                                                                                                                                                                                                                            Kato J., Misra T.K., Chakrabarty A.M.;
Algga3, a protein resembling eukaryotic histone Hl,
alginate synthesis in Beaudomonas aeruginosa.";
Proc. Natl. Acad. Sci. U.S.A. 87:2887-2891(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91008921; PubMed=1698761;
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Konyecsni W.M., Deretic V.;
                                                                                                                                                                 MEDLINE=90108714; PubMed=2514124;
                                                                                                                                                                                                                                                                                                                                                    STRAIN=8882;
MEDLINE=90222135; PubMed=2109318;
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STRAIN=PAO / PA02003;
                                                                                                                                                                                                                                                                       gene.";
Gene 84:31-38(1989).
                                                                                                                       SEQUENCE FROM N.A.
STRAIN=8822;
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SEQUENCE FROM N.A.
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ALGR3 OR
                                                                                    NCBI_TaxID=287;
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. Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                           Zhu Y., Han Y.; "Molecular Cloning of human hSTE cDNA."; Beijing Yi Ke Da Xue Xue Bao 31:531-531(1999)
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LINKER 12.
COIL 2A.
LINKER 2.
COIL 2B.
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COIL 1A.
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     Eukaryota; Metazoa;
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TISSUE=Brain;
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SEQUENCE FROM N.A.
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     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 PAAKTAAAKPAAKPAAKPVAKPTAK---PAAKTAAAKPAAKPAAKPAAKPAAKPVAKSAA 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 AKPAAKPAAKPAAKPAAKPVAAKPVAAKPAATKPATAPAAKPAATPSAPAASSAASATPA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 CLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 HSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSR 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 --bvoeslklaqgvckvkeaagkalesrkakpatkpaakaakpa-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%; Score 250.5; DB 1; Length 352;
55.4%; Pred. No. 0.0013;
(ve 42; Mismatches 170; Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFH HUMAN STANDARD, PRT, 1026 AA.
P12036, Q9UUS7; Q9UQ14;
D1-0CT-1989 (Rel. 12, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2010 (Rel. 41, Last annotation update)
16-MAR-2010 (Rel. 41, Last annotation update)
16-MAR-2010 (Rel. 41, Last annotation update)
Neurofilament triplet H protein (200 kDa neurofilament protein)
Neurofilament heavy polypeptide) (NP-H).
Homo sapiens (Human).
                                                                                                                                                            Alginate biosynthesis; Transcription regulation; Activator; DNA-binding; Repeat; Complete proceome.

CONFLICT 157 158 KP -> NA (IN REF. 1 AND 2).

CONFLICT 157 158 KP -> NA (IN REF. 1 AND 2).

CONFLICT 173 176 MISSING (IN REF. 1), 2 AND 3).

CONFLICT 181 188 188 T -> A (IN REF. 1, 2 AND 3).

CONFLICT 188 188 T -> A (IN REF. 1, 2 AND 3).

CONFLICT 223 224 KP -> NA (IN REF. 1 AND 2).

CONFLICT 266 267 PA -> HV (IN REF. 1, 2 AND 3).

CONFLICT 266 267 PA -> HV (IN REF. 1, 2 AND 3).

CONFLICT 266 267 PA -> HV (IN REF. 1, 2 AND 3).
                                                                                                                                                                                                                                                 KP -> NA (IN REF. 1)

MISSING (IN REF. 1)

A -> T (IN REF. 1)

A -> T (IN REF. 1)

A -> G (IN REF. 1)

T -> A (IN REF. 1, 2 AND 3).

KP -> NA (IN REF. 1, 2 AND 3).

T -> A (IN REF. 1, 2 AND 3).

T -> A (IN REF. 1, 2 AND 3).

T -> A (IN REF. 1, 2 AND 3).

T -> A (IN REF. 1, 2 AND 3).

MISSING (IN REF. 1, 2 AND 3).

KP -> NA (IN REF. 1, 2 AND 3).

KP -> NA (IN REF. 1, 2 AND 3).

KP -> NA (IN REF. 1, 2 AND 3).

KP -> NA (IN REF. 1, 2 AND 3).

KP -> NA (IN REF. 1, 2 AND 3).
  EMBL; M57551; AAA25703.1; -.
EMBL; M32077; AAA72068.1; -.
EMBL; AE004937; AAG08638.1; -.
PIR; A35630; A35630.
PIR; G82990; G82990; InterPro; IPR006970; PT.
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34490 MW;
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                                                                                                                                                      Pfam, PF04886, PT; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myajima N., Tanaka K.-I., Suyama M., Kikuno R., Hirosawa M., Myajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Myajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Trediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 5:35-364(1998).

In the res. Of the sequence of the sequence of the coding sequence of neuronal caliber. NF-H has an important function in mature axons that is not subserved by the two smaller NF proteins.

In the series a number of repeats of the tripeptide K.S-P, NFH is phosphorylated on a mumber of the series in this morif. It is thought that phosphorylation of NFH results in the formation of the maintenance of the mai
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-1- SIMILARITY: Belongs to the intermediate filament family.
SEQUENCE FROM N.A.
MEDLINE=88328981; PubMed=3138108;
Lees J.F., Shneidman P.S., Skuntz S.F., Carden M.J., Lazzarini R.-
"The structure and organization of the human heavy neurofilament
subunit (NF-H) and the gene encoding it.";
EMBO J. 7:1947-1955(1988).
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Query Match
      27;
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                                                                                                          EGCYEKVARLOKVETEIQRVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHD-----
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                   811 811 E -> A (IN REF. 1).
1026 AA; 112478 MW; 0879B6A0BD208C17 CRC64;
MISSING (IN REF. 3)
E -> A (IN BEF. 3)
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Last annotation update)
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(Rel. 34, Last sequ
(Rel. 43, Last anno
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01-0CT-1996
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                              SEQUENCE
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or RAF genes.
-!- DATABASB: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95096166; PubMed=7798308;
Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T.,
Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T.,
Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.;
"Tpr, a large coiled coil protein whose amino terminus is involved in activation of encogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
                                                                                              Mitchell P.J., Cooper C.S.;
"The human tyr gene encodes a protein of 2094 amino acids that he extensive coiled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
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                                           SEQUENCE FROM N.A.
MEDLINE=93064711; PubMed=1437155;
                                                                                                                                                                                                  [2] REVISIONS, AND CHARACTERIZATION
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Length 2349;

DB 1;

Score 245.5;

7.38;

Jakovcic S., Zak R.; structural and phylogenetic analysis of the chicken ventricular

Camoretti-Mercado B., Perlman D., Gupta

'Amino-acid sequence of the short subfragment-2 in adult chicken

MEDLINE=93039740; PubMed=1418675;

Watanabe B

myosin heavy chain rod."; J. Mol. Evol. 33:357-366(1991) [2]

Chem. Hoppe-Seyler 373:1045-1054(1992). FUNCTION: Muscle contraction.

cardiac muscle myosin.";

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1696
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                                                                                                                                                                   282 EKERLEQDLQQMQAKVRKLELDILPLQEANAELSEKSGMLQAEKKLLBEDVKRWKARNQH 1341
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                                                                                                                                                                                                                                                                                                                                                                                                                             24 RAQOMVEILISDENRNIRQELEGCYEKV---ARLOKVETEIORVSEAYENLVKSSSK---
                                                                                                                                                                                                                                                          -REALEKAMR-----NKLEGEIRRMHDFNRDLRER--LETANKQLAEKBYE----
                                                           Indels 201;
0.014;
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                        al Similarity 20.3%; Pred. No. 0.014 153; Conservative 127; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLRIQ-----OROGNCOPINVS----
                        Best Local Similarity
Matches 153; Conserv
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subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.

Pfan, PP01576; Myosin tail; 1. Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Multigene family.

InterPro, IPR002928; Myosin_tail.

NON TER

DOMAIN

EMBL; X59552; CAA42130.1; -. HSSP; P03437; IHTM.

-i-SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC).
-i-SUBCELULAR LOCATION: Thick filaments of the myofibrils.
-i-TISSUE SPECIFICITY: Ventricular muscle and traces levels in the atrium. Also transfent expression in skeletal muscle during fetal development and regeneration following freeze injury.
-i-DOMAIN: The rodilike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
-i-MISCELLANEOUS: Bach myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped

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187 KOVYVDKVEKMQQALVQLQAAC-----EKREQLEH--RLRTRLERELESLR-- 230
                                                                                                                                                                                                                                                                                                       135 NYESQREXEKURAEL---ATARSTNEDQR----RHIBIRDQALSNA-QAKVVKLEBELKK 186
                                                                                                                                              80
                                                                                                                                                               81 BKAMRNKLEGEIRRMHDFNRDLRERLETANKOLAEKEYEGS-----EDTRKTISQLFAK
                                                                                                                                                                                                                                                          22 VSRAQQMVBILSDENRNIRQELEGCYEKVARLQKVETBI-QRVSEAYENLVKSSSKREAL
                                                                                                  DB 1; Length 1102;
                                                                          2293668D049825DC CRC64;
   COILED COIL (POTENTIAL).
A -> T (IN REF. 1).
V -> A (IN REF. 1).
CS -> FAL (IN REF. 1).
H -> Q (IN REF. 1).
T -> R (IN REF. 1).
                                                                                                                    77; Mismatches 176;
                                                                                                 Score 242.5; DB Pred. No. 0.0086;
                                                                           128008 MW;
                                                                                                  7.2%;
                                                                                                              23.3%;
                                                                                                                          Matches 123; Conservative
1102
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114
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135 13
185 18
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, cardiac muscle isoform (Fragment).
Myosin seavy Chain, cardiac muscle isoform (Fragment).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves; Neognathae, Galliformes; Phasianidae, Phasianinae,

STANDARD;

CHICK

SC_CHICK

SEQUENCE OF 65-1102 FROM N.A. STRAIN-Broiler; TISSUE-Heart; MEDLINE-92130260; PubMed=1774788;

NCBI_TaxID=9031;

BL; X68879; CAA4874 R; S36326; S36326. RerPro; 128001026; tterPro; 128001026; tterPro; 128001026; tterPro; 128001026; tterPro; 128001026; tterPro; 1280017; tterPro; 1280017	Similarity 21 5; Conservativy MVELLSDENRNLRQ LIQAINEINVNIPQKLEGEIRRMHDP -KLEGEIRRMHDP -KLEGEIRRMHDP -KLEGEIRRMHDP -KLEGEIRRMHDP	Db 542 TATTSAAATTAAAPPALDI Qy 629 HRLSIPSUTCNPDKTDGFVF Db 602VPESSITADLLSGSGF
231 IQQRQGNCQPTNVSEYNAAAL		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL: X68877; CAA48748.1;

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ERLETANKOLAEKEY------EGSEDTRKTISQL 131
                                                                                                                                                                                                                                                                                                                                                                                                              TARSTNEDORRHIEIRDQALSNA---QAKVVKLEEELKKKQ 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :: | | :: | | :: | CKDALEIYKRFLITRMTRVSEPLKVADBVG-IDKGDIPDLT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEADMIKWEQKYLEENVWRHFALDAAATVAAQRDTTVISHS 305
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                                                                                                                                                                                                                                                                                                                       YEKVARLOKVETBIORVSBAYENLVKSSSKREALEKAMRN-
                                                                                                                                                                                                                                                   Score 242; DB 1; Length 915;
Pred. No. 0.0074;
8; Mismatches 282; Indels 166; Gaps
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POLY-ALA.
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Missing (in isoform Short).
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                                                             cing, Phosphorylation.
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                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
Hill W.D., Zhang L., Balin B.J., Sprinkle T.J., Spicer K.,
Gearhart D.A., The bovine neurofilament M subunit has a novel set of KSP repeats
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 7.2%; Score 241.5; DB 1; Length 810; al Similarity 20.6%; Pred. No. 0.0068; 152; Conservative 124; Mismatches 282; Indels 179;
                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
Neurofilament meddum polypeptide) (NF-M) (Fragment).
NEF3 OR NEFM OR NFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intermediate filament, Coiled coil, Neurone, Phosphorylation.

NON TER 1 1 296 ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
SIMILARITY: Belongs to the intermediate filament family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COIL 2B.
8 X 13 AA TANDEM REPEATS.
B8477D85560AC3F6 CRC64;
              810 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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COIL 2A.
LINKER 2.
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COIL 1A.
LINKER 1.
COIL 1B.
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InterPro, IPR001664; IF.
InterPro, IPR002957; Keratin_I.
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PRINTS; PR01248; TYPEIXERATIN.
PROSITE; PS00226; IF; 1.
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              STANDARD;
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Bovidae; Bovinae; Bos.
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172
176
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810 AA;
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83 AMRNKL-EGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKTISQLFAKNKESQRE 141

82 88

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------BBVKEEBAEEKBEK
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                                                                                  143 KDYLKTDISTALK-----EIRSQLESHSDONMHQAEEWFKCR--YAKLTEAAEQNK
                                                                                                                      202 VOLGAACEKREQLEHRLATRLERELESLRIQGRQGNCQPTNVSE---YNAAALMELLREK
                                                                                                                                               192 BAIRSAKBEIABYRRQLQSK-SIBLESVRGTKESLBRQLSDIBERHNHDLSSYQDTIQQL
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                                                                                                                                                                                            EERILALEADMIKWEQ-KYLEE----NVMRHFALDAAAIVAAQRDITVISHSPNISYDI
                                                                                                                                                                                                                                                                                                                                        356 LOQRSRKEPSK---TEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDKSWK
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Brain;
MEDLINE=89065087; PubMed=3143606;
MEDLINE=89065087; PubMed=3143606;
MEDLINE=89065087; PubMed=3143606;
Mennial sequence of the rat heavy neurofilament polypeptide (NF-H)
Identification of putative phosphorylation sites.";
FEBS Lett. 241:213-218(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Neurofilament triplet H protein (200 kDa neurofilament protein)
(Neurofilament heavy polypeptide) (NF-H) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                          348 EDEKSEMEEALTAITEELA-----VSVK----
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MEDLINE=88309090; PubMed=2457365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Neurofilaments usually contain three intermediate filament proteins: L, M, and H which are involved in the maintenance of neuronal caliber. NP-H has an important function in mature axons that is not subserved by the two smaller NF proteins. Perfer There are a number of repeats of the tripeptide K-S-P, NFH is phosphorylated on a number of the serines in this motif. It is thought that phosphorylation of NFH results in the formation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interfilament cross bridges that are important in the maintenance of axonal caliber.

of axonal caliber.

The Phosphorylation seems to play a major role in the functioning of the larger neurofilament polypeptides (NF-M and NF-H), the levels of phosphorylation being altered developmentally and coincident with a change in the neurofilament function.

SIMILARITY: Belongs to the intermediate filament family.

CAUTION: Ref. i sequence differs from that shown due to a frameshift in position 783.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89184647; PubMed=2928342;
MEDLINE=89184647; PubMed=2928342;
Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgaber D.,
Smulowitz M., Carroll Z., Banuel B.S., Breitner J., Rubin L.;
Mcloning of a cDNA encoding the rat high molecular weight
neurofilament peptide (NF-H): developmental and tissue expression in
the rat, and mapping of its human homologue to chromosomes I and
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                                                                             large neurofilament subunit (NF-H) of the rat: cDNA cloning and
                                                                                                                                                                                                                                                                          Robinson P.A., Wion D., Anderton B.H., Resolution of a CDNA for the rat heavy neurofilament polypeptide
Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L. Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF K-S-P
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-> P (IN REF. 2 AND 4).
1B0973C3F13EF76B CRC64;
                                                                                                                in situ detection.';
Biochem. Biophys. Res. Commun. 154:1099-1106(1988)
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                                                                                                                                                                                                              SEQUENCE OF 1-89 AND 243-313 FROM N.A
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EMBL; X13804; CAA32038.1; ALT_FRAME.
EMBL; M21964; AAA41695.1; -.
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PROSITE; PS00226; IF; 1.
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InterPro; IPR001664; IF.
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MEDDINB=93165729; PubMed=8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
                                                                                                                                                                                 227 ESLRIQORQGNCQPTNVSEYNAAALMELLREKEERILALEA-----DMTKWEQKYLEENV
                                                                                                                                                                                                                                                                                                         AAAITATAATITTTMVAAAPVAV-----AAAAAPAAAAAP----SPATAAAAV
                                                                                                                  19 QAQAQAEAR-----DALK-----CDVTSALREIRAQLEGHTVQSTLQSEEWFRVRLDRLS
                                                                                                                                                                                                                              69 BAAKVNTDAMRSAQEBITEYR-----RQLQARTTBLEALKSTKESLERQRSELED--
                                                                                                                                                                                                                                                                             282 MRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEBEEILMANKRCLDME----
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                                                                                       168 QALSNAQAKVVKLEBELKKKQVYVDKVEKMQQALVQLQA-ACEKREQLEHRLRTRLEREL
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Ballinger D.G., Xue N., Harshman K.D.;
"A Drosophila photoreceptor cell-specific protein, calphotin, binds
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                                            indels 169;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
  Length 831;
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Score 241.5; DB 1;
Pred. No. 0.007;
                                            Mismatches 1997
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         22.4%; F1.
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Best Local Similarity 22.49
Matches 131, Conservative
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                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BME outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 APIAVTPVAPPPTLASVQPATVTIPAPAPIAASVTPVASVAPPVVAAPTPPAASPVSTP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 VAVAQIPVAVSAPVAPPVAATPTPVVQIPVAAPVIATPPVAASAPTPAAVTPVISPVIAS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 ----ATAAAVSPAAAG-----QIPAAASVASAAAVAPSAAAAAAVQ--VAP--AA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 PAPVPAPALVPVPAP-AAAQASAP--AQTQAPTSAPAVAP----TPAPTPTPAVAQABVP 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 PST-PSPV--PPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 AITA-----TAAFI---TTTMVAAAPVAVA-----AAAAPAAAAAPSPATAA----
calcium and contains a leucine zipper.";

Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).

-!- FUNCTION: Might function as a calcium-sequestering "sponge" to regulate the amount of free cytoplasmic calcium. It binds 0.3 and of Calca+ per mole of protein.

-!- SUBGNIT: Homodimer (Probable).

-!- SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment.

-!- TISSUE SPECIFICITY: Somm and axons of photoreceptor cells of compound eyes and ocelli.

-!- DEVELOPMENTAL STAGE: Expressed early in photoreceptor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BECI YEAST STANDARD; PRT; 1157 AA.
P47068; P47067; QBXIF4;
P47068; P47067; QBXIF4;
P47068; P47067; QBXIF4;
P47068; P47067; QBXIF4;
P47068; P470681. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myosin tail region-interacting protein WTI1 (BBCI protein).
Myosin tail region-interacting protein WTI1 (BBCI protein).
BECI OR WILL OR YJLO20C/YJLO21C (OR J1305/J1286.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 240.5; DB 1; Length 865; 35.0%; Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I -> T (IN REF. 2).
V -> L (IN REF. 2).
D -> E (IN REF. 2).
; 2110417E0B0B7CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A -> AVAPAVVA (IN REF

I -> T (IN REF 2) .

T -> A (IN REF 2) .

P -> PP (IN REF 2) .

VQ -> AP (IN REF 2) .

VQ -> AP (IN REF 2) .

I -> V (IN REF 2) .

S -> T (IN REF 2) .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; LO2111; AAA28405.1; -. 
EMBL; LO5080; AAA28420.1; -. 
PIR; A47282; A47282. 
PIR; A47283; A47283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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84; Conserv
                                                                                                                                                                                                                                                                                                        development
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SEQUENCE
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LOAACEKREQLEHRLRTRLERELESLRIQORQ------GNCQP----TN 242
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-!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 LEABLATARSTNEDORRHIBIRDOALSNAOAKVVKLE---BELKKKKOVYVDKVEKMQQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Co-localizes with cortical actin patches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; S0003557; BBC1.
GO; GO:0005857; C:actin cortical patch (sensu Saccharomyces); IDA.
GO; GO:0017024; F:myosin I binding; IP1.
GO; GO:0017024; P:actin cytoskeleton organization and biogenesis;
GO; GO:0007010; P:cytoskeleton organization and biogenesis; IGI.
InterPro; IPR001452; SH3.
                                                                                                                                                                                    SEQUENCE OF 699-765 FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pohl T.M., Aljinovic G.; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases. FUNCTION: Involved in the regulation of actin cytoskeleton.
                                                                                                                                                                                                                                                                           Mochida J., Yamamoto T., Fujimura-Kamada K., Tanaka K.;
"The novel adaptor protein, Mtilp, and Vrplp, a homolog of
Wiskott-Aldrich syndrome protein-interacting protein (WIP), may
antagonistically regulate type I myosins in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.2%; Score 239.5; DB 1; Length 1157; 1.3%; Pred. No. 0.012;
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tive 99; Mismatches 256; Indels
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                                                                                                                  Jacq C.;
to the EMBL/GenBank/DDBJ databases.
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COILED COIL (POTENTIAL).
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .012;
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EMBL, Z49296, CAA89312.1; ALT_INIT.
EMBL, AF373805; AAL57239.1; -.
Germonline; 141636; -.
                                                                                                                                                                                                                                                      MEDLINE=21898311; PubMed=11901111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 775-1157 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in positions 729 and 732.
                                                                                                                                                                                                                                                                                                                                                                                                                         Senetics 160:923-934(2002).
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Best Local Similarity 21.3'
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M00326; SH3; 1.
PS50002; SH3; 1.
in; Coiled coil.
                                                                                                               To Van D., Perea J.,
Submitted (SEP-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1157 AA;
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                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356
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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Radaelin A., Schnada K., Shamada K., Shimada K., Sultana R., Takenaka Y. Taylor M.S., Taesdale R.D., Tomatra M., Vanda R.D., Werardo R., Watenabe Y., Walla R.D., Wannay Y., Watanabe Y., Wells C., Wang Y., Watanabe Y., Wells C., Wang Y., Watanabe Y., Walls C., Wang Y., Watanabe Y., Walls L., Wannay L., Yang L., Yang L., Alming L.G., Wangawa M., Yang I., Yang L., Yang L., Mari X., Kanu Z., Zavolan M., Zau Y., Carninci P., Hayatsu N., Sato K., Rainaba. M., Sakai K., Kamana Y., Radwa T., Fukuda S., Rara A., Hanhizume W., Imotani K., Ishinaya K., Arakwa T., Fukuda S., Rara A., Hanhizume W., Waterston R., Lander B.S., Rogers J., Ranalysis of the mouse transcriptome based on functional annotation of Stroylow B., Hayashizaki Y., Radwa K., Sahinayawa A., Rall-length COMRAS.";

R. Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573(2002).

C. FUNCTION: Binds phospholipid vesicles containing phosphatidylinositol 3-phosphate and participates in endosomal trafficking (By similarity).

C. SUBUNIT: Homodimer. Binds STX6. Binds RABSA RABSE RABSC and RABSA that have been activated by GTP-binding (By similarity).

C. SUBCRLUMAR LOCATION: Cytoplasmic and peripheral membrane protein associated with early endosomes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----DTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTLHAQIIE--- 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 RRHIEIRDQALSNAQAKVVKLEEELKKK------QVYVDKVEKMQQALVQLQAACEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 ---IMEKEÇQVADLQLKLSRLEBQLKEKVTNSTBLQHQLEKSKQQHQEQQALQQSATAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 RE---QLEHRLR------TRLERBLESL--RIQORGINCOPTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 -VSEYNAAALMEL-----LREKEERILALEADWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 PADPFAIVSRAQQM---VRILSDENRNLRQELE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%; Score 239; DB I; Length 790;
20.3%; Pred. No. 0.0083;
tive 96; Mismatches 187; Indels 216; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 -----KWEQKYLEENVMRHFALDAAATVAAQR------KWEQKYLEENVMRHFALDAAATVAAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             790 AA; 90539 MW; A167AE02CC2CA7BF CRC64;
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MGD; MGI:2442192; Beal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.1%
Best Local Similarity 20.3%
Matches 127; Conservative
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SEQUENCE
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529 KVSVQLDQLTAKFQEKQEHCIQLESHLKDHKEKHLSLEQKVEDLEGHIKKLEADALEVKA 588
                                                        349 -KDAMIKVLOOR-----SRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHS 393
                                                                                                                                                                    394 STLIGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKT---- 448
                                                                                                            589 SKEQALQSLQQQRQLSTDLBLRNAELSRELQEQEEVVSCTX----LDLQNKSBILENIK 643
                                                                                                                                                                                                                                Q61548; Q61547;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-MAR-2-104 (Rel. 43, Last amnotation update)
Clathrin coat assembly protein AP180 (Clathrin coat associated protein AP180) (91 kDa synaptosomal-associated protein Pl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Brain. Associated with the synapses.

DEVELOPMENTAL STAGE: Developmentally regulated in a pattern coincident with active synaptogenesis and synaptic maturation. DOMAIN: Possesses a three domain structure: the N-terminal 300 residues harbor a clathrin binding site, an acidic middle domain 450 residues, incernupted by an Ala-rich segment, and the C-terminal domain (166 residues).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 epsin N-terminal homology (ENTH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT). MEDLINE=92300439; PubMed=1607933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q61548~2; Sequence=VSP_000172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=261548-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                    449 GSRDCSTQTE-RGTESNKTAAVAPIS 473
                                                                                                                                                                                                                                                                                                                                         675 GDRMQAAVTELTAVKAOKDALLAELS 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M83985; AAA37587.1; -.
EMBL; M83985; AAA37586.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A44825; A44825.
MGI:109132; Snap91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A180 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNAP91.
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PIR; ;
MGD; ;
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210 CYNDGVINLLEKPPEMKKGQCKDALEIYKRFLTRWTRVSEPLKVARGVG-IDKGDIPDLT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                    97 --KLEGEIRRMHDFNRDLRERLETANKQLAEKEY-------EGSEDTRKTISQL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 LFNLSNFLDKSGSHGYDMSTFIRRYSRYLNEKAFSYRQMAFDFARVKKGADGVMRTM--- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 PAKNKESOREKEKURAELATARSTNEDORRHIEIRDQALSNA---QAKVVKLEEELKKKQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 VYYDKVEKMQQALVQL-QAACEKREQLEHRLRTRLERELESIRIQQRQGNCQPTNVSEYN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 AA--ALMELLREKEERILALBADMTKWEOKYLEENVMRHFALDAAATVAAQRDTTVISHS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 QAPSSLMETL---EQHINTLEG-----KKPGNNEGSGAPSPLSKSSPATTVT-S 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 PNTSYDTALEARIQKEBEBILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKBPS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 KTEQLSCWRPAKSLMSISNAGSGLLSHSSTLTGSPIMBEKRDDKSWKGSLGILLGGDYRA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | : | : | : | : 340 ----VSSAKPSSDLIDIQPDFSGAAAGAA----APVVPPSGGATAM----GDILGEDSLA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 EYVPST?SPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAATAA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 A-LSSVPCRAPISDPF-------APEP-SPFTTTEPASAS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 AITATAATITTTWVAAAPVAVAAA--AAPAAA-AAPSPATAAATAAAVSPAAAGQIPAAA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 ASITIAVIAVITEVDLFGDAFAASPGEAPASEGATAPATFAPVAAALD-ACSGNDPFAP 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 SVASAA-----AVAPSAAAAAV----OVAPAAPAPAPALVPVPAPAAQASAPA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 SEGSARAAPRIDLFAMKPPRISAPVVIPIASIAPPVPAIAPSPAPIAVAAIAAITIAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ASPATG 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 626 PGP------HRLSI------PSLTCNPDKTD------GPVFHSNTLE-RKTPIQI 661
                                                                                                                                                                                                                                                                                                                                                                                               45 LIQATNETNVNIPOMADTLFERATNSSWV--VVFKALVTTHHLMVHGNERFIQYLASRNT
                                                                                                                                                                                                                                                                                                                                                              28 MVBILSDBNRNLRQELEGCYEKVARLQKVETBIQRVSEAYENLVKSSSKRBALEKAMRN-
                                                                                                                                                                                                                                                                                                                             Conservative 105; Mismatches 281; Indels 192;
                                                                                                                                                                                                                                                                                        7.0%; Score 234; DB 1; Length 901;
20.8%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591 QTQAPTSAPAVAPTPAPTP----TPAVAQAEVP-----
                                                                                                                                                                                                                      (in isoform Short).
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24A98FBACE8DB881 CRC64;
InterPro; IPR001026; ENTH.
InterPro; IPR008943; Pl. bind_N.
Pfam; PF01417; ENTH; 1.
SMART; SM00273; ENTH; 1.
Coated pits; Alternative splicing; Phosphorylation.
DOMAIN 14 145 ENTH;
                                                                                                                                              POLY-ALA.
POLY-ALA.
                                                                                                                            POLY-THR
                                                                                                                                                                                                  POLY-SER
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                                                                                                                                                                                                                                                       901 AA; 91851 MW;
                                                                                                                                                                                                                                                                                                        20.8%;
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                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                            535
547
659
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715
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                                                                                                                                                                                                                                                       SEQUENCE
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arch completed: June 16, 2004, 19:17:44 b time : 20.5037 secs

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ALIGNMENTS

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P. Strucker.

X. MEDLINE=99397452; PubMed=10470851;
X. MEDLINE=99397452; PubMed=10470851;
X. MEDLINE=99397452; PubMed=10470851;
X. Tanaka A., Norani H., Nomura W., Ohara O.;
X. Tanaka A., Kotani H., Nomura W., Ohara O.;
X. Tanaka A., Kotani H., Nomura W., Ohara O.;
X. Tanaka A., Kotani H., Nomura W., Ohara O.;
X. Tanaka A., Kotani H., Nomura W., Ohara O.;
X. Tanaka A., Notani H., Nomura W., Ohara O.;
X. Tanaka A., Notani H., Nomura W., Ohara O.;
X. Tanaka A., Notani H., Nomura W., Ohara O.;
X. Tanaka A., Notani H., Nomura W., Millon M., EBC28B74427AD481 CRC64;
X. Mypothetical protein.
X. SEQUENCE 675 AA; 72540 MW, EBC28B74427AD481 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE FROM N.A.
MEDLINE-21157403; PubMed=11257124;
Troyanovsky B., Levchenko T., Mansson G., Matvijenko O., Holmgren L.;
Troyanovsky B., Levchenko T., Mansson G., Matvijenko O., Holmgren L.;
"Angiomotin. An angiostatin binding protein that regulates endothelial
"ell migration and tube formation.";
J. Cell Biol, 152:1247-1254 (2001).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                  O9HD27; Q9UPT1;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Angiomotin (Hypothetical protein KIAA1071).
675 A.A.
   PRT;
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Pred. No. 5.5e-109;
9; Mismatches 62;
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76.8%; Pred. no.
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                                                                                                                                                                                                                                                       EEELKKKQUYVDKVEKWQQALVQLQAACEKREQLEHRLRTRLERELESLR1QQRQGNCQP
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       MPRAQPSSASYQPVPADPPAIVSRAQQNVEILSDENRNLRQELEGCYEKVARLQKVETEI
                                                                                   QRVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEG
                                                                                                                                                          SEDTRKTI SOLPAKNKESORBKEKLEAELATARSTNEDORRHI EIRDOALSNAQAKVVKL
                                                                                                                                                                                                                                 EBELKKKKOVYVDKVEKWOOALVOLOAACEKREOLEHRLRTRLERELESLRIOOROGNOOP
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 891;
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EMBL; AP461135; AAL73436.1; -.
MGD; MGI:108440; Amot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95111 MW; C0544542A4CD608B CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=B6CBAP2; TISSUB=Placenta;
Troyanovsky B., Bratt A., Holmgren L.;
"Mouse angiomotin.";
Submitted (DEC-2001) to the EMBL/GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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SEQUENCE FROM N.A.
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01-MAR-2002 (
01-OCT-2003 (
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AMOT.
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                                                                                                        AKVVKLEBELKKKOVYVDKVEKMQQALVQLQAACEKREQLEHRLFTFLERELESLR1QQR
                                                                                                                                                                                                                                   GENCOPTIVVSEYNAAALMELLREKEERILALEADMIKWEQKYLEENVMEHFALDAAATVA
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                                                                                                                                                     SEDTRKTISOLFAKWK-----BSQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQ
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                          1 MPRAQPSSASYQPVPADPFALVSRAQQMV3ILSDENRNLRQELEGCYBKVARLQKVETEI
                                            ORVSEAYENLVKSSSKREALBKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEG
Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 82;
 Indels
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STISSUB=Muscle;
Strabberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8IY63;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to anglomotin like 1.
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498 AA;
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Best Local Similarity
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Kawai U., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawai T., Shinaqawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

Arakwa T., Hara A. Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A saito T., Okazaki Y., Gojobori T., Bono H., Kasukwa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Soffelli D., Bojunga N., Carninci P., Gariboldi M.,

Blake J., Soffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchonni L., Mashina J., Mazzarelli J., Momberts P.,

A Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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                                                                                                                                  RVSEAYENLVKSSSKREALEKAMRNYLEGEIRRMHDFNRDLRERLETANKQLAEKEYEGS
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                                                                                 Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 956;
                                                                                 Indels
 AAH37539.1; -.
\A, 106574 MW; 6F47AE3A13816E95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                               43.3%; Score 1448; DB 4;
62.0%; Pred. No. 2.7e-55;
ive 83; Mismatches 82;
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                                                                Best Local Similarity 62.0
Matches 292, Conservative
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   BC037539; AAF
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                   SECUENCE
                                                  Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
  ŝ
                                      "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki
                                                                                                                                                                                                   Length 882;
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                                                                                   EMBL; AKO16526; BAB30287.1; -.
MGD; MGI:1922973; Amoctl.
GO; GO:0005923; C:tight imction; IDA.
GO; GO:005823; C:tight imction; IDA.
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                                                                                                                                                                                                 41.8%; Score 1400; DB 11;
58.2%; Pred. No. 3e-53;
iive 80; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1338; DB 4;
Pred. No. 7.9e-51;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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nes 236; Conservative
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Matches
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                                                                                                                                           RELEGLRIOOROGNOOPINVSEYNAAALMELLREKERERILALEADMIKWEOKYLEENVMR 283
                                                                                                                                                                                              241 HFAWMAATAAARRDTFIINHSRNGSYGESSEBAHWQEEEEVVQANRRCQDWEYIIKNL 300
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                                                                                                                                                                                                                          HAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIM 402
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                          103
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                                                                                                                 44 EGCYEKVARLOKVETEIORVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMIDFNRDLR
                                    ERLETANKOLAEKEYEGSEDTRKTISOLFAKNKESOREKEKEKLEAELATARSTNEDORRHI
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      Gaps
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AMOTE2.

Buks musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 772;
      14;
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32.6%; Score 1090.5; DB 11; Lengtl
Best Local Similarity 50.4%; Pred. No. 7.1e-40;
Matches 244; Conservative 71; Mismatches 118; Indels
      71; Indels
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to angiomotin like 2.
       Mismatches
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       75;
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        Conservative
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Q8K371;
01-OCT-2002 (
01-OCT-2002 (
01-OCT-2003 (
        2695
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                                                                                                                        AATVAAQRDTTVISHSPNTSYDTALEARIQKEEERILMANKRCLDMEGRIKTLHAQIIEK 349
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523
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annotation
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.5%; Score 1087.5; DB 11; Length 463; 52.7%; Pred. No. 5.6e-40; ive 68; Mismatches 103; Indels 41;
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MEDLINE-C57BL/G17 IISSUBE-Aorta, and Vein;
MEDLINE-22354683; PubMed=12466851;
The FAMTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II
Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BNBI, AKO40912; BAC30740.1;
PIR; PT0534; PT0534.
MGD; MGT:192286; Amot12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 AA; 51758 MW; 2F7BE52FBC8B1678 CRC64;
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                             400 PAHTKHGSRDGSTQTD-GPADNTSACLA 426
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             443 SAHSKTGSRDCSTQTERGTESNKTAAVA
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Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRABYVPS---TPSPVPPSTPLL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TOGWOG----LVSSEROTDARPAGDRVPAEEPPATAPL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
                                                                                                                          ------TQGWQG----LVSSERQTDARPAGDRVPAEEPPATAPL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 IRRMHDFWRDIRERLETANKQLAEKBYEGSEDTRKTISQLFAKWKESQREKEKLEABLAT 151
251 EADMTKWEQKYLEERAMRQFAMDAAJTAAAQRDTTLIRHSPQPSPSSSF-----NEGL 303
                              LMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR=C2546461 TISSUE=Body;
MEDLINE=C3546461 TISSUE=Body;
The FANTOM Consortium,
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
wanalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.';
Nature 420:563-573 (2002).
BAGD: AR077535; BAG36853.1;
PIR: PT0534; PT0534.
MGD; MGI:1929286; Amortl2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARSTNEDQRRHIEIRDQALSNAQAKVVKLEEELKKKQVYVDKVEKNQQALVQLQAACEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQLELRIRTRIRGELKALRAQQRQTGTLAGGGSHGGSARISALRISEQLREKESQILAL
                                               GSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPS---TPSPVPPSTPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 LSDENRNLRQELEGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREALEKAMRNYLEGE
                                                                                                                                                                                                                                                                                                                                                                      AMOTL2.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 32.1%; Score 1075.5; DB 11; Length 463; al Similarity 52.2%; Pred. No. 1.8e-39; 234; Conservative 70; Mismatches 103; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 AA; 51733 MW; 0394E0334ACFA17E CRC64;
                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                              400 PAHTKHGSRDGSTQTD-GPADNTSACLA 426
                                                                                                                                                           SAHSKTGSRDCSTQTERGTESNKTAAVA 470
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                                                                                                                                                                                                                                                                        PRT;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 23
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290 AATVAAQRDITVISHSPNTSYDTALEARIQKEEEEILMANKRCLDWEGRIKTLHAQIIEK 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAMIKVIQQRSRKBPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMBEKRDDK 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 VETBIORVSEAYENLVKSSSKREALEKAMRNKLEGBIRRMHDFNRDLRERLETANKQLAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 -----GNCQPTNVSEYNAAALMELLREKEERILLALEADMTKWEQKYLEENVMRHFALDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 TGTLAGGGGSHOGSAELSALRISEQLREKEEQILALEADMIKWEQKYLEERAMRQFAMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 GWQG----LVSSERQTDARPAGDRVPAEEPPATAPLPAHTKHGSRDGSTQTD-GPADNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 PSSASYQPVPADDPPAIV----SRAQQMVEILSD-----ENRNLRQELEGCYEKVARLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 PSSFGPPAVEGPPSAQATLGSAHLAQMETVLRENARLQRDNERLQREBESTSEKAGRIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 KEYEGSEDTRKTISQIFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 KVVKLEBELKKKOVYVDKVEKMOQALVOLOAACEKREQLEHRLRTRLERELESLRIQORO
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                                                                                                                                                      Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rođentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.0%; Score 1069.5; DB 11; Length 49.8%; Pred. No. 4.3e-39; tive 71; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                           SECURNCE FROM N.A.

Kessler R., Brunet J.-F., Van Meir E.G.;
"Murine homolog of the human LCCP gene. Variant 1.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF175967; AAD56362.2; -.
MGD; MAI:1229286; Amot12.

NON_TER
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01-WAY-2000 (TrEMBLrel. 13, Created) 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2003 (TrEMBLrel. 23, Last annotation update) Angiomotin-like protein 2 variant 1 (Fragment) AMOTIE.
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157

217 175 289 397 545

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359
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Best Local S:
Matches 238
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Q96E99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 LPGNHRHQEWESRLKVLHAQILEKDAVIKVPQQRSRKDPGKATQ-GTLWPAKSVPSIFAA 362
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                                                                                                                                                                                                                                                                                                                                                                                                                 ARSTNEDORRHIEIRDOALSNAOAKVVKGEEELKKKOVYVDKVEKMOOALVOLOAACEKR
                                                                                                                                                                                                                                                                                                     LSDENRNIROELEGCYEKVARLOKVETE I QRVSEAYENI VKSSSKREALEKAMRNKLEGE
                                                                                                                                                                                                                                                                              Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1918_TaxID=9606;
              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Angiomotin-like protein 2 variant 2.
AMOTIZ.
MARTINECULUS (Mouse).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11 NCBL TaxID=10090;
                                                                                                                                                                                                                                                  463;
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                                                                                                                                                                                                                                                  DB 11; Length
                                                                                                                                                                                                                                                31.9%; Score 1066.5; DB 11; Lengtl
ilarity 52.0%; Pred. No. 4.5e-39;
Conservative 68; Mismatches 106; Indels
                                                                                                                                                              Kessler R., Brunet J.-F., Van Meir E.G., Kessler R., Brunet D.C.P., Van Meir E.G., Straint 2.";
"Murine homolog of the human LCCP gene. Variant 2.";
Submitred (AUG-1999) to the BNBL/GenBank/DDBJ databases.
EMBL, AF175968, AADS6363.1;
SEQUENCE 463 AA, 51778 MW; 1493D08034FBBD70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 SAHSKIGSRDCSTQTERGIESNKTAAVA 470
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                                                                                                                                                                                                                                                                 Local Similarity
les 233; Conserv
                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     Query Match
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SEQUENCE FROM N.A.
TISSUE-Alloblastoms.

Kessler R., Brunet J.-F., Van Meir B.G.;
"Leman coiled-coil protein (LCCP) identified from a glioblastoma cell

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  265
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                                                                                                                                                                                                                                                                     123
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                                                                                                                                                                                                                                                                                                                             SEAYENLVKSSSKREALBKAMRNKLEGEIRRMHDFNRDLRBRLETANKQLAEKBYBGSED
                                                                                                                                                                                                                                                                                                                                                   239 OPTNVSEYNAAALMELLREKEERILALBADYTKWEQKYLBENVWRHFALDAAATVAAQRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSRKEPSKTEQLSCWRPAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                   206 SQDWVAKLIAQSYBQQQBQBKLEREMALIRGAIBDQRRRABILEQALGNAQGRARAEBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 LKKKQVYVDKVBKMQQALVQLQAACEKREQLEHRLRTRLBRELESLRIQQRQ-----GNC
                                                                                                                                                                                                                                             13 PVPADPFAIVSRAQQMVBI-----LSDENRNLRQELEGCYEKVARLQKVBTIQRV
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                         64;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BCD11454; AAH11454.1; ... Hypothetical protein.
                                                                                                                                                                  Length
                            databases
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466 AA; 51814 MW; AlablaFS47CD197C CRC64;
                                                                                                                           569 AA; 62877 MW; 8950E515DD10C215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                  31.2%; Score 1045; DB 4; 46.9%; Pred. No. 4.9e-38;
line expression library.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ of EMBL, AR175966; AAD56361.2;
InterPro; PR000408; Reg_chr_condens.
PROSITE; PS00626; RCCl_2; 1.
NOW TER 1 1 1
SEQÜENCE 569 AA; 62877 MW; 8950E515DD10C21
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                                                                                                                                                                                     ; Pred. No. 4.9e 79; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 48.8
Matches 234; Conservative
                                                                                                                                                                                         al Similarity 46.9
238; Conservative
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SEQUENCE FROM N.A.
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238

614

554

494

298

674

358

418 764 821

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124 EKREGLELELETELEGELKALRAGORGAPGGSSGSGGSPELSALRLSEGLREKEEGIL 183
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                                                                                                                                                                                                                                                                                     419 LGGDYRABYVPS------TPSPVPPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAV 469
SEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKOLAEKRYEGSED 123
                   184 IKKKQVYVDKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESIRIQQRQ-----GNC
                                                                                                                                                    765 SSSERQTADAPARLTTADRAPTEEPVVTAPP--AAHAKHGSRDGSTQTDGPPDSTSTCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKREQLEHRLRTRLERELESIRIQORO - - - - GNCOPTNVSEYNAALMELLREKEERIL
                                                                                    239 QPTINVSEYNAAALMELLREKEERILALEADMIKWEQKYLEENVMRHPALDAAAIVAAQRD
                                                                                                                                                                                                                                                                     TTVISHSPNTSYDTALEARIQKERBEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQ
                                                                                                                                                                                                                                                                                                                                                           89 EGEIRRAHDFWRDIRERLETANKOLAEKEYEGSEDTRKTISOLFAKWKESOREKEKLEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 LATARSTNEDORRHIEIRDOALSNAOAKVVKLEEBILKKKOVYVDKVEKMOOALVOLQAAC
                                                                                                                                                                                                                                                                                                                                       RSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTGSPIMEBKRDDKSWKGSLGIL
                                                                  124 TRKTISQLFAKNKESQREKEKLEABLATARSTNEDQREHIBIRDQALSNAQAKVVKLEEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 25.9%; Score 867.5; DB 4; Length 402; al Similarity 47.3%; Pred. No. 1.7e-30; 200; Conservative 62; Mismatches 106; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 AA; 44234 MW; SAD4ADF0E8A83676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last
Hypothetical protein (Fragment)
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TISSUB-Panorceas;
Strausberg R.;
Submitted (VAR-2002) to the
EMBL, EC025981; AAH25981.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
                                                                                                                                                                        212 BOLBHRIRTRLERELESIRIQORQ-----GNCOPTNVSEYNAAALMELLREKEERILALE 266
                                                                                                                                                                                                                                                                                        267 ADMTKWEGKYLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEREEIL 326
                                                                                                                                                                                                                                                                                                          327 MANKRCLDWEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCWRPAKSLMSISNAG 386
                                                                                                                                                                                                                                                                                                                                                                                                                           387 SGLLSHSSTLTGSPIMBEKRDDKSWKGSLGILLGGDYRAEYVPS-----TPSPVPPS 438
                                                                                    151
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                     91
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DNA Res. 6:63-70 (1999).

EMBL; AB021206; BAA76833.1;

Genew; HGMC:17812, AMOTL2.

PROSITE; PS00626; RCC1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 PVPADPFAIVSRAQQMVEI-----LSDENRNLRQELEGCYEKVARLQKVETBIQRV
                       LSDENRNLRQELEGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREALBKAMRNKLEGE
                                       92 IRRMHDFNRDIRERIETANKOLARKEYEGSEDTRKTISQLFAKNKESQREKEKIRARAT
                                                                                                                                                      152 ARSTNEDORRHIEIRDQALSNAQAKVVKLEEELKKKQVYVDKVEKMQQALVQLQAACEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.1%; Score 1040.5; DB 4; Length 46.6%; Pred. No. 1.2e-37; tive 80; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          859 AA; 94325 MW; SAF7E211E4CF738D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein KIAA0989 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel, 12, (TrEMBLrel, 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 46.6%
237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999
01-NOV-1999
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Best Local Si
Matches 237;
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                     32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 VTAPP--AAHAKHGSRDGSTQTDGPPDSTSTCL----PPEPDSLLGCSSSQRAASLDSV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 LEENVARHFALDAAATVAAQRDTTVISHSPNTSY-DTALEARIQKEEBRILMANKRCLDM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 LEBSTIRHFANNAAATAAAERDTTINHSRNGSYGESSLEAHIWQBEBEVVQANRRCQDM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 LTGSPIMEEXRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPL-----LSAHS 446
184 ALEADMIKWEQKYLEERAMRQFAMDAAATAAAQRDTILIRHSPQPSPSSSF-----NE 236
                                                    384 NAGSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPS-----TPSPV 435
                                                                                                                                                                                                         -----GTOGWOG----LSSSEROTADAPARLTTDRAPTEEPV 333
                                                                                                                                                                                                                                                             436 PPSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAP-----VAAAATAAAITAT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RIRTWLERELDALRTQQKHGNGQPANMPEYNAPALLELVREKEBERILALBADMTKWEGKY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 RIRTRIERELESIRIQOROGNOOPTNVSEYNAAALMELLREKEERILALBADMTKWEQKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
DKFZP43402216.
DKFZP43402216.
Bukryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.1%; Score 738.5; DB 4; Length 326; Best Local Similarity 59.4%; Pred. No. 5.5e-25; Matches 152; Conservative 47; Mismatches 44; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1)—
SEQUENCE FROM N.A.

TISSUE—Testis;
TOSUE—Exertis;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL83333; CAD38693.1; --
Hypotherical protein.
NON TER 1
SEQUENCE 326 AA; 35950 MW; 5E28183735E67B56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                            296 AAAAA----
                                                                                                                                                                                                                                                                                                                                                                    491 AAT 493
                                                                                                                                                                                                                                                                                                                                                                                                                     ATS 389
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SNDNO
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earch completed: June 16, 2004, 19:14:52 ob time : 65.7139 secs

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June 16, 2004, 19:06:57; Search time 17:8313 Seconds (without alignments) 2265.920 Million cell updates/sec
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1 BSNKTAAVAPISVPAPVAAA......QASAPAQTQAPTSAPAVAPT 143
                                                                                                                                                                                                                                                                                                                                                                                    1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    stal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             1586107 segs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                          inimum DB seq length: 0
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rfect score:
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geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* geneseqp2004s:*

A Geneseq 29Jan04:* i: genesemini

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		SP	Ö	Aay54053 A variant	o.		m	m	0	Human	Aab35408 Human 07C	ᅋ			Nove	Abu90134 Novel hum	Abu96436 Novel hum	Abu99045 Novel hum	Abu98260 Novel hum	Abu91966 Novel hum	Abu85270 Novel hum	Abo00409 Novel hum	Abu88960 Novel hum	Abo06456 Novel hum	Abu95516 Novel hum	Abu95206 Novel hum
SUMMARIES	ID		AAY54054	ABP43965	AAY54053	AAY54052	AAE37918	ABU21693	AB023523	ABB78540	ABR92087	AAB35408	ABR57561	ABB66631	ABB71319	ABU88255	ABU90134	ABU96436	ABU99045	ABU98260	ABU91966	ABU85270	ABO00409	ABU88960	ABO06456	ABU95516	ABU95206
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40	Query Match		100.0	100.0	100.0	100.0	97.6	34.1	33.0	32.9	32.5	32.5	31.5	ų.	14	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	•
	Score	1 1 1 1 1	663	663	663	663	647	226	218.5	218	215.5	215.5	209	205.5		205.5				205.5							
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	Novel	Novel	Abu82045 Novel hum	Novel	Abo05231 Novel hum		Abb71039 Drosophil	Abg04954 Novel hum	Aaw26540 Trypanoso	Aay23307 Trpanosom	Abg20119 Novel hum	Abbs9024 Drosophil	Aaw06913 T. cruzi						
ABU90754	ABU93916	ABU86190	ABU82045	ABU07906	ABU94226	AB000099	ABU87110	ABU91351	ABU90444	ABU97035	AB005231	ABU39775	ABB71039	ABG04954	AAW26540	AAY23307	ABG20119	ABB59024	AAW06913
ø	9	ø	9	v	v	9	ø	ø	ø	v	ø	ø	4	4	~	(1	4	4	7
1743	1743	1743	1743	1743	1743	1743	1743	1743	1743	1743	1743	329	1013	806	442	442	2724	477	262
31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31,0	31.0	31.0	30.9	30.8	30.4	30.2	30.2	30.2	30.2	29.7
205.5	205.5	205.5	205.5	205.5	205.5	205.5	205.5	205.5	205.5	205.5	205.5	205	204.5	201,5	200.5	200.5	200.5	200	197
26	27	28	29	30) E	32	33	34	32	36	37	38	66	40	41	42	43	44	45

ALIGNMENTS

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kringle domain; angiostatin; plasminogen receptor;
angiogenesis-related disease; tumor; diabetes; rheumatoid arthritis;
inflammatory disease; psoriasis; chronic inflammation; intestine; asthma;
obesity; gene therapy; angiostatin-binding domain; Big-3.
                                                                 angiogenesis-associated protein; plasminogen; ABP-1;
                                                   Angiostatin-binding domain of ABP-1, designated Big-3.
       AAY54054 standard; protein; 143 AA
                                     (first entry)
                                     27-MAR-2000
AAY54054
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98SE-00002130. 98US-0089266P. 98SE-00004372. 98US-0114386P. 99WO-EP004109 W09966038-A1 Homo Bapiens 11-JUN-1999; 15-JUN-1998; .5-JUN-1998; .7-DEC-1998; 29-DEC-1998; 23-DEC-1999

(PHAA) PHARMACIA & UPJOHN AB Troyanovsky B; Holmgren L,

WPI; 2000-106099/09.

Novel human protein useful for treating angiogenesis associated diseases or disorders.

Claim 6; Page 49; 58pp; English.

The present sequence represents the angiostatin-binding domain, designated Big-3, of a human angiogenesis-associated protein. The protein binds an N-terminal fragment of plasminogen. The ABP-1 protein is designated ABP-1, and binds the first 4 kringle domains (KI-K4) and/or kringle 5 (K5) of plasminogen. These four kringle domains comprise angiostatin. The ABP-1 protein acts as a receptor for plasminogen. A polymorphic variant of ABP-1 is also described, in AAV54053. ABP-1 can be used to manufacture medicaments for treating angiogenesis-related

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arthritis, and even some inflammatory diseases such as psoriasis, chronic inflammation of the intestine, asthma, etc. The protein may also be able to treat and cure, or prevent, obesity. The ABP-1 DNA can be used in gene
diseases or disorders, such as tumor conditions, diabetes, rheumatoid
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                                                                                                                                                                        1 ESNKTAAVAPISVPAPAAATAAAITATAAIITTIMVAAAPVAVAAAAAPAAAAPSPA 60
                                                                                                                                           ESNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAAPAAAAPSPA 60
                                                                                        Gaps
                                                                                       ..
                                                          Length 143;
                                                                                     0; Indels
                                                       ; Score 663; DB 3;
; Pred. No. 5.1e-39;
0; Mismatches 0;
                                                                                                                                                                                                                                   121 AAAQASAPAQTQAPTSAPAVAPT 143
                                                                                                                                                                                                                                                    100.08;
                                                                       100.08;
                                                                                    Matches 143; Conservative
                                                     Query Match
Best Local Similarity
therapy techniques
                            Sequence 143 AA;
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ABP43965 standard; protein; 479 AA 3P43965

ABP43965;

(first entry) 26-FEB-2003

Unidentified protein seguence.

anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation; Neuroprotective; immunomodulator; cancer; chromosome X; cytostatic; wlnerary.

Homo sapiens.

WO200231111-A2,

18-APR-2002

11-OCT-2001; 2001WO-US027760.

12-OCT-2000; 2000US-00687527

(HYSE-) HYSEO INC.

Ren F; Zhao QA, Zhang J, RT; Asundi V, , Drmanac Liu C, Zhou P, As: Yang Y, Wehrman T, Xue AJ,

WPI; 2002-426278/45. N-PSDB; ABQ61209.

New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or inflammation.

Claim 20; SEQ ID # 868; 357pp + Sequence Listing; English.

The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, volnerary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as untritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,

Novel human protein useful for treating angiogenesis associated diseases

Claim 5; Page 46-49; 58pp; English.

or disorders.

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amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polymucleotides of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                         266 ESNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAAAAAAAPSPA 325
                                                                                                                                                                                                                                                          61 TAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPAPAPALVPVPAP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kringle domain, anglostatin, plasminogen receptor, anglogenesis-related disease, tumor, diabetes, rheumatoid arthritis; inflammatory disease, psoriasis, chronic inflammation, intestine, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148. 150
/note= "these residues are either Glu-Leu-Ala or Thr-Thr-
                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A variant of an angiogenesis-associated protein which binds plasminogen.
                                                                                                                                                                                                    1 ESNKTAAVAPISVPAPAPATAAAITATAATITTTMVAAAPVAVAAAAAPSPA
                                                                                                                                                                        Gaps
                                                                                                                                                                        .
0
                                                                                                                                            Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; angiogenesis-associated protein; plasminogen; ABP-1;
                                                                                                                                                                        Indels
                                                                                                                                           100.0%; Score 663; DB 5;
100.0%; Pred. No. 1.6e-38;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Asn, Ser, Asp
                                                                                                                                                                                                                                                                                                                   121 AAAQASAPAQTQAPTSAPAVAPT 143
                                                                                                                                                                                                                                                                                                                                            386 AAAQASAPAQTQAPTSAPAVAPT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   AAYS4053 standard; protein; 675 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHAA ) PHARMACIA & UPJOHN AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0089266P.
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                                                                                                                                                          al Similarity 100.
143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obesity; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-106099/09
                                                                                                                Sequence 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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7-DEC-1998;
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                                                                                                                                            Query Match
                                                                                                                                                            Best Local
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Claim 4; Page 43-46; 58pp; English.

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The present sequence represents a polymorphic variant of a human angiogenesis-associated protein which is able to bind an N-terminal fragment of plasminogen. The native protein, described in AMY54052, is designated ABP-1, and binds the first 4 kringle domains (KI-K4) and/or kringle 5 (X5) of plasminogen. These four kringle domains comprise angiostatin. The ABP-1 protein acts as a receptor for plasminogen. The angiostatin-binding domain of the ABP-1 protein is described in AAY54054. ABP-1 can be used to manufacture medicaments for treating angiogenesis-related diseases or disorders, such as tumor conditions, diabetes, related diseases or disorders, such as tumor conditions, diabetes, psorials, chronic inflammation of the intestine, asthma, etc. The protein may also be able to treat and cure, or prevent, obesity. The ABP-1 DNA can be used in gene therapy techniques
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Sequence 675 AA;

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TAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAVQVAPAAAAPAPAPALVPVPAP 120
                                                                                                                                              581
                                                          80
                                                                                                                                 1 ESNKTAAVAPISVPAPVAAAATAAAITATAATITTTWVAAAPVAVAAAAAAAAAPSPA
                              Gaps
                           ..
Length 675;
                           0; Indels
100.0%; Score 663; DB 3;
100.0%; Pred. No. 2.2e-38;
                             0; Mismatches
                                                                                                                                                                         121 AAAQASAPAQTQAPTSAPAVAPT 143
                             Conservative
Query Match
Best Local Similarity
Matches 143; Conserv
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                                                                                                                                               522
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Y54052 SULT

AAAQASAPAQTQAPTSAPAVAPT 604

Ę AAYS4052 standard; protein; 675

AAY54052;

(first entry) 27-MAR-2000

An angiogenesis-associated protein which binds plasminogen.

kringle domain; angiostatin; plasminogen receptor; angiogenesis-related disease; tumor; diabetes; rheumatoid arthritis; inflammatory disease; psoriasis; chronic inflammation; intestine; asthma; Human; angiogenesis-associated protein; plasminogen; ABP-1; obesity; gene therapy

Ношо

W09966038-A1

23-DEC-1999.

99WO-EP004109 11-JUN-11999;

98SE-00004372. 98US-0114386P. 98SE-00002130. 98US-0089266P. 15-JUN-1998; 29-DEC-1998; 15-JUN-1998; 17-DEC-1998;

(PHAA) PHARMACIA & UPJOHN AB

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Тгоуалочвку

Holmgren L,

WPI; 2000-106099/09

N-PSDB; AAZ45329

Novel human protein useful for treating angiogenesis associated diseases or disorders.

20-DEC-2001; 2001US-0340747P. 20-DEC-2001; 2001US-0342761P. 15-JAN-2002; 2002US-0349705P. 06-FEB-2002; 2002US-0354764P. 12-FEB-2002; 2002US-0356216P.

(INCY-) INCYTE GENOMICS INC.

04-DEC-2002; 2002WO-US039133

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The present sequence represents a human angiogenesis-associated protein which is able to bind an N-terminal fragment of plasminogen. The protein is designated ABP-1, and binds the first 4 kringle domains (KI-K4) and/or kringle 5 (K5) of plasminogen. These four kringle domains comprise angiostatin. The protein acts as a receptor for plasminogen. The angiostatin-binding domain of the ABP-1 protein is described in AAY54054. A polymorphic variant of ABP-1 is also described, in AAY54053. ABP-1 can be used to manufacture medicaments for treating angiogenesis-related diseases or disorders, such as tumor conditions, diabetes, rheumatoid arthritis, and even some inflammatory diseases such as peoriasis, chronic inflammation of the intestine, asthma, etc. The protein may also be able therapy techniques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 ESNKTAAVAPISVPAPVAAAATAAAITATAATITTTIMVAAAPVAVAAAAAPAAAAPSPA 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cell growth, differentiation and death protein; CGDD; leukaemia; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; muscular disorder: myotonic dystrophy; catatonia; endocrine disorder; diabetes; Grave's disease; cancer; immunological disorder; scleroderma; systemic lupus erythematosus; allergy; Crohn's disease; renal disorder; gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis; cardiovascular disorder; atheroselerosis; hepatic disease; transgenic; transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic; dermacological; immunosuppressive; cerebroprotective; anticonvulsant; antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSNKTAAVAPISVPAPVAAAATAAAITATAATITTTWVAAAAPVAVAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                     Length 675;
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                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 663; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.2e-38;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AAAQASAPAQTQAPTSAPAVAPT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              582 AAAQASAPAQTQAPTSAPAVAPT 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CGDD-7 protein.
                                                                                                                                                                                                                                                                                                     Sequence 675 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                      death (GGDD) proteins and polymucleotides encoding them. The sequences of the invention are useful in diagnosing, preventing and treating disorders associated with an abnormal expression or activity of GDDD such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. parkinson's disease, Alzheimer's endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g. leukaemia, cervical or breast cancers), immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allorgies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. doodpasture's syndrome), infections (e.g. viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis) protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis) and hepatic diseases (e.g. cirrhosis). The polymucleotides can be used to create humanised animals or transgenic animals to model human diseases. The invention is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  780 ESNXTAAVAPISVPAPVAAAATAAAITATAAIITSIMVAAAPVAVAAAAAAAAAAPSPA 839
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                          Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel cell growth, differentiation and death (CGDD) proteins and polymiclestides andoding the
                                                                                                                                                                                                                     New CGDD polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of CGDD, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
  Emerling BM, Kable AE, Elliott VS;
Gorvad AE, Yue H, Lee EA, Becha SD, Ta
Lee S, Ison CH, Hafalia AJA, Tran B;
are R, Gandhi AR, Gletzen KJ, Bhatia U;
Ho A, Zheng W;
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Pred. No. 4.1e-37;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #7220.
                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 220-222; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AAAQASAPAQTQAPTSAPAVAPT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU21693 standard; protein; 354 AA.
                             Swarnakar A, Lee S, I, Lee S, Khare R, S, Blake JJ, HO A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.9
Matches 140; Conservative
       Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burkholderia fungorum
                                                                                                                                                   WPI; 2003-532903/50.
N-PSDB; AAD57227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 993 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGDD-7 protein
Griffin JA,
Marquis JP,
Tran UK, Swa
Sprague WW,
Burrill JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2003
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the invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cancillated by the antisense antisense antisense antisense the specification is inhibited by the antisense antisense nucleic acid; (3) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding cap bytypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation, or that that inhibits cellular proliferation of an identifying a gene required for callular proliferation or the biological pathway required for proliferation required gene or its gene product lies or a gene on which the terecompound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids required for callular proliferation to isolate candidate molecules for rational for equired for proliferation to isolate candidate molecules for rational for equiring for proliferation in cells and every programs, or for screening homologous nucleic acids required for required for proliferation and the remember of surpersonal sequence is encoded by one of required for proliferation and the professed of the present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 ATABAVSPAAGGIPAAASVASAAAVAPSAAAAAVQVAPAAPAVPAPAPALVPVPAPAAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVA-AAAAPAAAAABSPATAA
                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Indels
                                                                                                                                                              Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

34.1%; Score 226; DB 6;
Best Local Similarity 46.4%; Pred. No. 2.5e-08;
Matches 64; Conservative 18; Mismatches 52;
                                                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 49617; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 QASAPAQTQAPTSAPAVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 GA-ATARTRRPGCAAGAA 211
                                                                                                                                                                    Malone C,
Carr GJ,
06-SEP-2001; 2001US-00948993.
25-07-2001; 2001US-0342928P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                         2003-029926/02
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                                                                                                                                                                                                                                                                  N-PSDB; ACA25563
                                                                                                                                                                    Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB023523
ID ABO
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AEO23523 standard; protein; 309 AA.

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The present invention relates to a method for identifying candidate proteins in pathogens useful as anti-infectives. The invention discloses a computational method which involves the calculation of several sequence attributes and their subsequence manalysis results in the identification of outlier proteins in different pathogens. The method is useful for the identification of outlier proteins (e.g. virulence proteins, antigens or proteins used as drug targets) in pathogenic organisms. The method of the invention provides reproducible results as it does not depend on the variable biochemical characterisation of proteins. ABO23500-ABO23501 represent outlier proteins identified from different pathogenic organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 КТАААКРААКРААКАААКРААК---КРААККТААКТААКРААКРААКРААКРАТАК
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 ATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAQVAPAA-PAPVPAPALVPVPAPAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KTAAVAPISUPAPVAAAATAAAITATAATITTTMYAAAPVAVAAAAAAAAAAPSPATAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying candidate proteins useful as anti-infectives involves matching outlier protein sequences with protein sequences in databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                            Candidate protein identification; pathogen; anti-infective; outlier protein; virulence protein; antigen; drug target protein; pathogenic organism; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhimarao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.0%; Score 218.5; DB 7
45.0%; Pred. No. 7.2e-08;
iive 8; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nandi T,
                                                                                                                    Pseudomonas aeruginosa outlier protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Page 37-38; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB78540 standard; protein; 103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brahmachari SK, Ramachandran S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001US-00820843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001US-00820843
                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRAH/) BRAHMACHARI S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAMACHANDRAN S.
                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RAMA/) RAMACHANDRA!
(NAND/) NANDI T.
(BHIM/) BHIMARAO C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                          US2003039963-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 309 AA;
                                                           04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUE-2002
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AB023523;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The present invention describes synthetic genes encoding plant gums and other hydroxyproline (Hyp)-rich glycoproteins (HRGPB) and the nucleic acids that encode them. The nucleic acids, proteins and methods from the present invention may be used to produce HRGPB, repetitive proline-rich proteins (RRPRP) and arabinoglactan-proteins (ARBPB) in plants via recombinant methodologies, Also described is the expression of synthetic genes designed from repetitive peptide sequences, such as glycoproteins (Including the peptide sequences of gum arabic glycoproteins (ARBS)730 to ABJS1849 and ABBP8401 to ABB78544 represent sequences used in the exemplification of the present invention
                          Plant, Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
HRGP; repetitive proline-rich protein; RFRP; arabinogalactan protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 AAAPVAVAAAAAAAAAAABAASPATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 арар-арарарарарарарарарарарарарара---рарар-арарарарарара
                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids and proteins useful for producing hydroxy-proline rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Ala-Pro-Ala-Pro construct related protein sequence SEQ ID NO:240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cervical cancer; cervical cancer marker; cancer therapy; detection; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer cell marker encoding cDNA SEQ ID NO:83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 VOVAPA APAPVPAPALVPVPAPAAQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.9%; Score 218; DB 5; 57.1%; Pred. No. 2.8e-08; iive 3; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR92087 standard; protein; 2701 AA
                                                                                                                                                                                                                                                                                                                                                                                                                         Example 25; Fig 18; 326pp; English
                                                                                                                                                                                                                                    12-APR-2000; 2000US-00547693.
                                                                                                                                                                                                      12-APR-2001; 2001WO-US012336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             glycoproteins in plants.
                                                                                                                                                                                                                                                                                                                             WPI; 2002-041307/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                   (UYOH-) UNIV OHIO
                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL51829.
                                                                                                                                                                                                                                                                                                 Kieliszewski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2002101075-A2.
                                                                                                                                         WO200178503-A2.
                                                               AGP; plant gum.
                                                                                             Acacia senegal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2002.
                                                                                                                                                                       25-OCT-2001
                                                                                                            Synthetic.
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Best Local S
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13-JUN-2001; 2001US-0298155P.

12-JUN-2002; 2002WO-US018638

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ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I) given in ABR92047 to ABR92164. A higher level of expression of (I) than normal indicates the presence of cervical cancer. Also described: (1) a certor (II) containing (I); (2) a host cell (III) containing (I); and (3) assessing (M1) whether a patient is afflicted with cervical cancer, comprising comparing the level of expression of a marker in a patient's sample, and the normal level of expression of the marker in a patient's cample, and the normal level of expression of the marker in a control non-cervical cancer sample, where a significant increase in the level of expression of the marker in the patient's sample relative to that in the cervical cancer. (I) has cytostatic activity, and can be used in gene therapy and in vaccines. (I) is useful in detecting, characterising, characterising and treating human cervical cancers. (I) may also be used in various prognostic and diagnostic assays, pharmacogenomics and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 07CG27 gene; chromosome 1; HPC1 region; prostate cancer; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ATABATAAAVSPAAAGQIPAAASVASAAAVAPSAAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 TAAVAPISVPAPVAAAATA-----AAITATAATITTIMVAAAPVAVAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.5%; Score 215.5; DB 6; Length 2701; Best Local Similarity 34.1%; Pred. No. 8.8e-07; Matches 58; Conservative 25; Mismatches 48; Indels 39;
                                                                                                                                                                   Kamatkar S;
                                                                                                                                                                   Zhao X, Monahan JE,
X, Hoersch S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 233-239; 386pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB35408 standard; protein; 2819
13-JUN-2001; 2001US-0298159P.
                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human 07CG27 gene protein
                                                                                                                                                                   Schlegel R, Chen Y,
Gannavarapu M, Glatt
                                                                                                                                                                                                                                                               WPI; 2003-156967/15.
N-PSDB; ACF12869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 SP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200116291-A2.
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                                                                                                                                                               Schlegel
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The present invention provides the protein and coding sequences of the human 070227 oncogene. This gene is found at the HPC1 region of chromosome 1. The sequences can be used in the diagnosis and identification of treatments for prostate cancer. The present sequence is
                                                                                                                                                                      Novel human prostate cancer marker gene termed as 07CG27 gene, useful for screening mutations in the gene in diagnosis of a predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, Antiallergic, Dermatological, Antiinflammatory, Gene therapy, mast cell activation, allergic hypersensitivity, asthma; mastocytosis; seasonal rhinitis; urticaria; atopic dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                       5 TAAVAPISVPAPVAAAATA-----AAITATTATITTTWVAAAPVAVAAAAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1901 TASVPLAPASASAPAPAPTPVSAPNPAP-----PAPAQTQAQTHKPVQNP 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 AAAVOVAPA---APAPVPAPAIJVPVPAPAAAQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 215.5; DB 4; Length 2819; 34.1%; Pred. No. 9.2e-07; ive 25; Mismatches 48; Indels 39;
                                                                                                      Rommens JM
                                                                                                       Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR57561 standard; protein; 1259 AA
                                                                                                                                                                                                                             Claim 1; Page 91-99; 99pp; English.
                                                              (MYRI-) MYRIAD GENETICS INC. (HOSP-) HOSPITAL FOR SICK CHILDREN
           25-AUG-2000; 2000WO-US023291
                                    99US-0151049P
                                                                                                      Favtigian SV, Swedlund B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 34.1
Matches 58; Conservative
                                                                                                                                 2001-226682/23
                                                                                                                                                                                                                                                                                                               the 07CG27 protein
                                                                                                                                                                                                                                                                                                                                         Sequence 2819 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 SP----
                                                                                                                                               N-PSDB; AAF28060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                     27-AUG-1999;
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                                                                                                                                                                                                      cancer.
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Thomis D,

Medley Q,

Nocka K,

(UNIO) UCB

WPI; 2003-381640/36

27-SEP-2002; 2002WO-EP010897. 01-OCT-2001; 2001US-0325536P

WO2003029464-A2

10-APR-2003.

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for diagnosing or treating allergic ma, seasonal rhinitis, urticaria, atopic dermatitis

New MC21 gene, useful for hypersensitivity, asthma,

or mastocytosis.

N-PSDB; ACC80175

9

Gaps

14;

Length 1259; 54; Indels

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The present invention relates to novel human sequences associated with mast cell activation (ACC80172-ACC80179 and ABR57558-ABR57565). The coding sequences are useful for diagnosing or treating allergic hypersensitivity, asthma, seasonal rhinitis, urticaria, atopic dermatitis or mastocytosis
                                                                                                                                                                                                                                       PATAAATAAAVSPAAAGQIPAAASVASAAAAAAAAAAAQVAP---AAPA--PVPAPA 113
                                                                                                                                                                                                                                                                                   2 SNKTAAV---APISVPAPVAAAATAAITATATITTIMVAAAPVAVAAAAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 26685; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 26685.
                                                                                                                                                                             31.5%; Score 209; DB 6; 39.3%; Pred. No. 1.2e-06; ive 23; Mismatches 54
                                                                                                                                                                                                                                                                                                                               LVPVPAPAAAQASAPAQTQAPTSAPAVAPT 143
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                                                              Claim 17; Page 101-106; 120pp; English.
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                           Query Match
Best Local Similarity 39.34
Matches 59; Conservative
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                                                                                                                                                        Sequence 1259 AA;
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interactions.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and

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                                                                                                                                                                                                                                                                                                 135 VIATPPVAASAPTPAAVTPVVSPVIATPPVVPANTTVPVAAPVAAVPAAVPVVAPVIAPA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent expable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
                                                                                                                                                                                                                                                                                 96
                                                                                                                                                                                                                                                  74
cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                      ----TTTMVAAAPVAVAAA
                                                                                                                                                                                                                                               16 APVITPSAVAAPVOVVSPAAVAPAAPIAVITPVAPPPILASVOPAIVTIPAPAPIA-AAS
                                                                                                                                                                                                                                                                            49 AAPAAAAAP----SPATAAATAAAVSPAAAGQIPAAAS-----VASAAAVAPSAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                       51; Gaps
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                                                                                                                                                            Length 842;
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                                                                                                                                                                                       Indels
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                                                                                                                                                                                       55;
                                                                                                                                                          DB 4;
                                                                                                                                                     31.0%; Score 205.5; DB 4
36.9%; Pred. No. 1.5e-06;
tive 12; Mismatches 55
                                                                                                                                                                                                                  6 AAVAPISVPAPVAAAATAAAITATAATI----
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                      Best Local Similarity 36.9
Matches 69; Conservative
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genes from Drosophila and
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                                                                                                                          Sequence 842 AA;
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                                                                                                                                                                6 AAVAPISVPAPVAAAATAAAITATAATI-------TTTMVAAAPVAVAAA 48
                                                                                                                                                                                       16 APVITPSAVAAPVQVVSPAAVAPAAPIAVIPVAPPPILASVQPAIVIIPAPAPIA-AAS 74
                                                                                                                                                                                                                     49 AAPAAAAAP----SPATAAATAAAVSPAAAGQIPAAAS-----VASAAAVAPSAAAA- 96
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                   51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, secreted and transmembrane protein: PRO; gene therapy, tumour necrosis factor-alpha release; TMR-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour, adrenal tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
                                                                                                       Query Match
31.0%; Score 205.5; DB 4; Length 864;
Best Local Similarity 36.9%; Pred. No. 1.5e-06;
Matches 69; Conservative 12; Mismatches 55; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane PRO polypeptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABU88255 standard; protein; 1743 AA.
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970S-0063121P.
970S-0063540P.
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                                                                                 Sequence 864 AA;
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24-007-1997;
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12-DEC-1997;
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98US-0089653P.
98US-0089908P.
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98US-0090246P.
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22-UN-1998; 98US-0090254P.

24-UN-1998; 98US-0090432F.

24-UN-1998; 98US-0090441P.

24-UN-1998; 98US-0090441P.

24-UN-1998; 98US-0090441P.

25-UN-1998; 98US-0090441P.

25-UN-1998; 98US-0090461P.

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25-UN-1998; 98US-0090461P.

25-UN-1998; 98US-0090694P.

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25-UN-1998; 98US-0090694P.

26-UN-1998; 98US-0099063P.

27-SEP-1998; 98US-010049P.

28-SEP-1998; 98US-010049P.

28-SEP-1998; 98US-010049P.

28-SEP-1998; 98US-010049P.

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28-SEP-1998; 98US-010049P.

28-SEP-1998; 98US-0100908P.

28-SEP-1998; 98US-0100908P.

28-SEP-1998; 98US-0100908P.
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                                                                                                                                                                     5 TAAVAPISVPAPAAAA-TAAAITATATITTTMYAAAPVAVAAAAAAAAAAPSPATAA
                                                                                                                                                    1; Gaps
                                                                                                                                Length 1743
                                                                                                                              Query Match
31.0%; Score 205.5; DB 6; Length
Best Local Similarity 57.6%; Pred. No. 2.9e-06;
Matches 57; Conservative 6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                         Movel human secreted and transmembrane PRO protein #3.
                                                                                                                                                                                                          ABU90134 standard; protein; 1743 AA
 98US-0101786P.
98US-0102240P.
98US-0102330P.
98US-0102331P.
98US-0102570P.
98US-0102570P.
98US-0102684P.
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Matches 57; Conservative 6; Mismatches 35; Indels 1;
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 65
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APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Wichael J.
APPLICANT: Lodes, Wichael J.
APPLICANT: Smith, John W.
APPLICANT: Smith, John W.
APPLICANT: Smith, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
TITLE OF INVENTION: OF T. CRUZI INPECTION
TITLE OF INVENTION: OF T. CRUZI INPECTION
TITLE OF INVENTION: OF T. CRUZI
CURRENT APPLICATION NUMBER: US/09/256,976
CURRENT APPLICATION NUMBER: US/09/256,976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.2%; Score 200.5; DB 3; Length 442; 45.8%; Pred. No. 1.7e-08; tive 6; Mismatches 64; Indels 7
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
PILING DATE: 13-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGRIT INFORMATION:
NAME: Maki, David J. 1392
REGISTRATION NUMBER: 210121.422C2
TELECOMMUNICATION INFORMATION:
TELEPRICE (206) 622-4900
TELEPRICE (206) 682-6031
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AAAQASAPAQTQAPTSAPAVAP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/09256976
Patent No. 6419933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.8
Matches 65, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-993-674A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 ААРРАКТААРРАКАААРРАКАААРРАКАААРРАКААААРАКАААРАКАААРР-АКАААР 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SNKTAAVAPISVPAPAAATAAAITATITATATITITMVAAAPVAVAAAAAAAAAPSPAT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: Smith, John 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.2%; Score 200.5; DB 3; Length 442; Best Local Similarity 45.8%; Pred. No. 1.7e-08; Matches 65; Conservative 6; Mismatches 64; Indels 7;
                                                                                                                  COUNTRY: Seattle
COUNTRY: Washington
COUNTRY: Washington
COUNTRY: Washington
COUNTRY: William Country
ZIP: 98104-7092
COMPUTER READ-BLE FORM:
MEDIUM TYPE: FORD
COMPUTER: IBM PC COMPatible
COUNTRY APPLICATION NATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: IS-APR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: MAXI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.422C1
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPAK: (206) 622-601
INPORMATION POR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AAAQASAPAQTQAPTSAPAVAP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 981.04-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALINE
OPERATING SYSTEM: PC-DOS/MS-DK
SOFTWARE: Patentin Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
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JS-08-834-306-52
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110 BDAAAAAAKOKAAAKKAAAPSGKKSAKAAIAPAKAAAAPAKAAAAP-AKAAAAPAKAAA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Steiry, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION
NUMBER OF SEQUENCES:
ADDRESSEE: SEED and BERRY ILP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Mashington
COUNTRY: USA
ZIP: 981.04-7032
COMPUTER: BIP PC Compatible
COMPUTER: BIP PC Compatible
COMPUTER: PIPPEY ELOSS/MS-DOS
SOFTWARE: PER PC COMPUTER:
MEDIUM TYPE: Floppy disk
COMPUTER: BIP PC Compatible
COMPUTER: BIP PC Compatible
COMPUTER: BIP PC COMPUTER:
MEDIUM TYPE: Floppy disk
COMPUTER: BIP PC COMPUTER:
MEDIUM TYPE: Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/929,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Indels
                                                                                                         CCUNTRY: USA
ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FEW PC COMPATIBLE
COMPUTER: FEW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,379A
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.406
FRIEDEHOMS: (206) 682-6031
FRIEDEHOMS: (206) 682-6031
FIREDEHOMS: CAPARACTERISTICS:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
I-WACTH: 262 amino acids
     :: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.7%; Score 197; DB 1;
44.3%; Pred. No. 1.9e-08;
tive 8; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 LVPVPAPAAQASAPAQTQAPTSAPAVAP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08929414
Patent No. 5942403
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 44.3
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                     Washington
                      STREET: bocc
        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-403-379A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 КТААРРАКТААРРАКАААРРАКАААРРАКААЭРРАКАААРРАКАААРАКАААРРАКАААРР-АКАА 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ATAAATA-AAVSPAAAGQIPAAASVASAAAVAPSAAAAAAQVAPAAPAPAPVPAPALVPVP 118
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                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Steven G.
APPLICANT: Joudes, M. Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300_Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 219;
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Patent No. 575662
GENERAL INFORMATION:
GAPPLICANT: Reed, Steven G.
TITLE OF INVEXTION: COMPOUNDS AND METHODS FOR THE DETECTION
TITLE OF INVEXTION: OF T. CRUZE INFECTION
NUMBER OF SEQUENCES: 9
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/557,309B FILING DATE: 14-NOV-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: 210121.422 RESERVENCE/DOCKET NUMBER: 31,392 RESERVENCE/DOCKET NUMBER: 210121.422 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 INFORMATION POR SEQ ID NO: 54: SEQUENCE CHRACTERISTICS: LENGTH: 219 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery Match 29.9%; Score 198.5; DB 2; Best Local Similarity 45.1%; Pred. No. 1.2e-08; Matches 65; Conservative 4; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 APAAAQASAPAQTQAPTSAPAVAP 142
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| |: ||: || 11
412 PAKAAAPPAKAAAPPAKAAAAP 433
                                                                                                                                                        Sequence 54, Application US/08557309B; Patent No. 5916572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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IS-08-557-309B-54
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PREVENTION OF
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                                                                                                                            1 ESNKTAAVAPISVPAPVAAA----ATAAAITATAATITTTMVAAAAPVAVAAAAAAAA
                                                                                                                                                                                                                56 APSPATAAATAAAVSPAAAGOIPA--AASVASAAAVAPSAAAAAVQVAPAAPAPVPAPA
                                                                                                                                                                      111 EDAAAAAKOKAAAKKAAAPSGKKSAKAAIAPAKAAAPPAKAAAP-AKAAAAPAKAAA
                                                                                   12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/08834306
Patent NO. 6054135
GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 197; DB 3; Length 263;
Pred. No. 1.9e-08;
8; Mismatches 63; Indels
                                         Length 263;
                                                                                   63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIAL
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                       Score 197; DB 2;
Pred. No. 1.9e-08;
8; Mismatches 63
                                                                                                                                                                                                                                                                                                     114 LVPVPAPAAQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                 230 ---ATAPAKA-ATAPAKAAAPAKAATAP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILLING DATE: 15-APR-1997
CLASSIFICATION: 424
ATTORNEY AGENT TINCERMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C1
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,306
FILING DATE: 15-APR-1997
CLASSIFICATION: 424
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                                         29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 263 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 44.33
Matches 66; Conservative
                                     Query Match
Best Local Similarity 44.3*
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Colun
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
TELEFAX: (
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US-08-557-309B-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 EDAAAAAAKQKAAAKKAAAPSGKKSAKAAIAPAKAAAAPAKAAAP-AKAAAAPAKAAA 168
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51, Application US/08557309B

Datent No. 5916572

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Hodes, Michael J.
APPLICANT: CAPPURES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 Length 262;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DOS/MA-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14 NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                               Score 197; DB 2;
Pred. No. 1.9e-08;
8; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 ---ATAPAKA-ATAPAKAAAAPAKAATAP 253
                                         NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.406C1
TELECOMMUNICATION INFORMATION:
TELEPRONE: (206) 622-4900
TELEPKX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPRENCE/POCKET VMBER: 210121.422
TELECOMMUNICATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.3%;
Matches 66; Conservative
  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                         : 262 amino acids
amino acid
                                                                                                                                                                                                                                                     ; TOPLICGY: linear
; MOLECULE TYPE: protein
US-08-929-414-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDALL
STREET: 6300
CITY: Seattle
THE WASHINGTON
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino a STRANDEDNESS: TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                       LENGTH:
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111 EDAAAAAAKOKAAAKKAAAPSGKKSAKAIAPAKAAAAPAKAAAP-AKAAAPAKAAA 169
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                                     APPLICANT: SMICH, JOHN M.
APPLICANT: SMICH, JOHN M.
APPLICANT: MICHAEL J. Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
TITLE OF INVENTION: OF T. CRUZI INPECTION
FILE REPREMENCE: 210121.4223
CURRENT APPLICATION NUMBER: US/09/256,976
CURRENT PILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 95
SOCTWARE: PATENTIN VET. 2.0
ENG JD NO 51
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ESNKTAAVAPISVPAPVAAA-----ATAAAITATAATITTTMVAAAPVAVAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SSNKTAAVAPISVPAPVAAAATAAA-ITATAATITTTMVAAAPV----AVAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 197; DB 4; Length 263;
Pred. No. 1.9e-08;
8; Mismatches 63; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Where any Xaa is an independently selected amino; OTHER INFORMATION: acid
US-09-256-976-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION DAMES W., STRAUSBERG, ROBERT L., WILSON, SUSAN D., POPP, SHARON H., STRAUSBERG, ROBERT L., WILSON, SUSAN D., POPP, SHARON H., STRAUSBERG, SUSAN L., RUFF, MICHAEL D., AUGUSTINE, PATRICIA C., DANPORTH, HARRY D.

TITLE OF INVENTION: GRNETICALLY ENGINEERED COCCIDIOSIS
SPOROZOITE 21.5 KB ANTIGEN, AC-6B
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18,07/581,693
FILING DATE: 12-28F-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 215,162
FILING DATE: 19-JUN-1988
FILING DATE: 19-JUN-1988
FILING DATE: 05-JUL-1984
FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.4%; Score 195; DB 6; Length 180; ilarity 43.0%; Pred. No. 1.8e-08; Conservative 8; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 LVPVPAPAAQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ATAPAKA-ATAPAKAAAAPAKAATAP 254
                         APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.3%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                ORGANISM: Trypanosoma cruzi
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Laca 65; Conserve
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                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                    APPLICANT: Ecughton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: Mossill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
PILING DATE: 18-DEC-1997
CLASSIPICATION: 424
ATTORNEY/ABORTINORMATION:
NAME: Maki, David J.
REGISTRAFION NUMBER: 31.392
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.7%; Score 197; DB 3;
44.3%; Pred. No. 1.9e-08;
tive 8; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 LVPVPAPAAQASAPAQTQAPTSAPAVAP 142
  LVPVPAPAAQASAPAQTQAPTSAPAVAP 142
                              ---ATAPAKA-ATAPAKAAAAPAKAATAP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 ---ATAPAKA-ATAPAKAAAAPAKAATAP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210121.422C2
                                                                                                                                                            Sequence 51, Application US/08993674A
Patent No. 6228372
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application US/09256976
Patent No. 6419933
GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 21
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 263 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.3
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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NAME: Michaels, Christopher A
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 786 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 118 No CITY: Ithaca STATE: NY COUNTRY: USA
                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                          HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09103429A
Sequence 4, Application US/09103429A
Patent No. 6187558
BAPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: AND And Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6187558th Tioga
                                                                                                            PACENT NO. 5482709

APPLICATI: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON, SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.; SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.; AUGUSTINE, PATRICIA C.; LANNORTH, HARRY D.

TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH SELICITS ANTIGENEDES AGAINST AVIAN COCCIDIOSIS
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,432
FILING DATE: 08-NOV-1993
FILING DATE: 08-NOV-1993
FILING DATE: 12-SEP-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-ULL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.4%; Score 195; DB 6; Length 180; 43.0%; Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 VPAPALVPVPAPAAQASAPAQTSAPA 139
                     147 KPGGHAAASTAAKAAQEKAAKAANAATAATA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 KPGGHAAASTAAKAAOEKAAKAANAATAATA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
PAPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.01
Matches 65; Conservative
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                                                                            RESULT 13
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORAGNISM: Trichoplusia ni
TISSUE TYPE: peritrophic membrane
S-09-103-429A-3
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5 TARVAPISVPAPVAAAATAAAITATAATI------TTTMVAAAPVAVAAA--AAPAA 53 Query Match

28.0%; Score 185.5; DB 3; Length 786;
Best Local Similarity 37.6%; Pred. No. 4.4e-07;
Matches 59; Conservative 8; Mismatches 69; Indels 21; Gaps

earch completed: June 16, 2004, 19:13:24 ob time : 6.94377 seca

equence 99, Appl equence 19, Appl equence 19, Appl equence 14, Appl equence 13, Appl equence 27, Appl Sequence 27, Appl Sequence 37, Appl Sequence 33, Appl Sequence 335, Appl Sequence 17, Appl

Sequence Sequence Sequence Sequence

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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: All and Secretary and Applicant
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ROCODING THE SAME
TITLE OF INVENTION: ACIDE ROCODING THE SAME
TITLE OF INVENTION: ACIDE ROCODING THE SAME
FILE REPERRENCE: P3430R.IC.227
CURRENT FILING DATE: 2002-06-28
FUOR REAT PRILING DATE: 2002-06-28
FUOR Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 75
LENGTH: 4640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tahangagnentahahahanggearantenenenthahahahahahahahahahahahaha 4552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TAAVAPISVPAPVAAAATAAA---ITA----TAATITTIMVAAAPVAVAAAAAAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 37.6%; Score 249.5; DB 14; Length 4640; I Similarity 51.4%; Pred. No. 2.8e-08; 74; Conservative 7; Mismatches 56; Indels 7;
US-10-141-759-99
US-10-140-864-99
US-10-184-644-149
US-10-184-644-149
US-10-184-644-149
US-10-184-644-27
US-10-184-644-27
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US-10-184-644-27
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US-10-140-865-37
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US-10-140-864-483
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US-10-184-644-335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 75, Application US/10184644; Publication No. US20030044930A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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CORGANISM: Homo Sapien
US-10-184-644-75
  US-10-184-644-75
                                                                                                                                                                                             239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 75, Al
Sequence 169, 1
Sequence 169, 1
Sequence 37, Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_RBW PUBL.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUBL.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

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                    version 5.1.6
- 2004 Compugen Ltd.
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US-10-184-644-169
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US-10-141-761-99
US-10-141-885-99
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                                                                                                                       - protein search, using sw model
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Result

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TYPE: DNA
CORGANISM: Homo Sapien
US-10-184-634-169
                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo Sapien
US-10-184-644-169
                                                                                                                                                                      LENGTH: 2846
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Peul J.
APPLICANT: Goddwaki, Peul J.
APPLICANT: Goddwaki, Peul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Mood, William I.
APPLICANT: Matanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: ALADAGAZA
APPLICANT: ALADAGAZA
APPLICANT: ALADAGAZA
APPLICANT: ALADAGAZA
APPLICANT: Chinyemyton: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PAJORICATI
CURRENT APPLICATION NUMBER: US/10/184, 634
CURRENT FILING DATE: 2002-06-29
PTIOR APPLICATION NUMBER: US/10/184, 634
CURRENT FILING DATE: EMPORATOR CONTRACTOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 4640;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8e-08;
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                                                                                                            118 PAPAAQASAPAQTQAPTSAPAVA 141
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                                                                                                                                                                                                                                                                                                                                      Sequence 75, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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JS-10-184-634-75
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APPLICANT:
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Granabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: ApplicANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C2.7
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
ENGTH: 2846
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                                                                                                                                                                                                                                                                              Query Match 37.6%; Score 249; DB 14; Length 2846; Best Local Similarity 50.4%; Pred. No. 1.9e-08; Matches 68; Conservative 8; Mismatches 59; Indels 0;
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CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 169
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Best Local Similarity 50.4%; Pred. No. 1.9e-08;
Matches 68; Conservative 8; Mismatches 59;
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Publication No. US20030068684A1
GENERAL INFORMATION:
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See Palm or File Wrapper
                                                                                                                              Score 247; DB 12;
Pred. No. 1.8e-08;
7; Mismatches 52;
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Pred. No. 1.8e-08;
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CURRENT FILING DATE: 2002-04-15
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Publication No. US20030068794A1
GENERAL INFORMATION:
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                                                                                                                              Query Match
Best Local Similarity 53.5%;
Matches 68; Conservative
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APPLICANT: Beresini, Maureen
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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Smith, Victoria
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 99
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; SEQ ID NO 99
; LENGTH: 1904
; TYPE: DNA
; ORGANIEN: Homo Sapien
US-10-142-426-99
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CRGANISM: Homo Sapien
US-10-123-155-99
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Watanabe, Colin E.
APPLICANT: Watanabe, Colin E.
APPLICANT: Wood, William I.
TITLS OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC FILLS OF INVENTION: ACIDS ENCODING THE SAME
FILLS OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT APPLICATION NUMBER: US/2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 170
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C224
CURRENT APPLICATION NUMBER: US/10/142,426
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Pred. No. 1.9e-08;
8; Mismatches 59; Indels 0
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                                           Sequence 37, Application US/10063685
Publication No. US20030180909A1
GENERAL INFORMATION:
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50.4%;
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                                                                                                        APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APFLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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Goddard, Audrey
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Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Best Local Similarity 50.4'
Matches 68, Conservative
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Filvaroff, Ellen
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CORGANISM: Homo Sapien
JS-10-063-685-37
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC30
                                                                                   15 APVAAAATAAAITATAATITTTMVAAAPVAVAAAAAAAAAAAABSPATAAATAAAVSPAAA
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75 GQIPAAASVASAAAVAPSAAAAAVQVAPAAPAPAPAPALVPVPAPAAAQASAPAQTQAP 134
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                                                          APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C166
CURRENY APPLICATION NUMBER: US/10/140,472
CURRENY PTLING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 1904
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.3%; Score 247; DB 14; Length 1:
Best Local Similarity 53.5%; Pred. No. 1.8e-08;
Matches 68; Conservative 7; Mismatches 52; Indels
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Pred. No. 1.8e-08;
7; Mismatches 52;
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Publication No. US20030148432A1
GENERAL INFORMATION:
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Best Local Similarity 53.5%;
Matches 68; Conservative 7
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Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
Watanabe, Colin K
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Gurney, Austin L.
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Filvaroff, Ellen
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                                  Wood, William
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CORGANISM: Homo Sapien
US-10-140-472-99
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ORGANISM: Homo Sapien
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APPLICANT: Watanabe Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBRICE: P3310R1G323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT APPLICATION THE 2002-05-15
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Pred. No. 1.8e-08;
7; Mismatches 52; Indels 0.
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                                                                                                                                  Sequence 99, Application US/10146731 Publication No. US20030129692A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.5%;
Matches 68; Conservative
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Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
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Gurney, Austin L.
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Filvaroff, Ellen
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
US-10-146-731-99
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Sequence 99, Application US/10137871
Publication No. US20030207350A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                               Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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                      Gao,Wei-Qiang
Gerritsen,Mary E.
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Filvaroff, Ellen
Gao, Wei-Qiang
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Goddard, Audrey
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: Wood, William
                                                                                Godowski, Paul J.
Gurney, Austin E.
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Gurney, Austin L.
                                                                                                                             Sherwood, Steven
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Smith, Victoria
                                                                 Goddard, Audrey
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US-10-158-790-99
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APPLICANT:
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APPLICANT:
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1770 BACBABATBABGTGBABTCCCBABABABABABABABABABABABABABABABA 1829
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                                                              75 GQIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPAPAPALVPVPAPAAAQASAPAQTQAP 134
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FILE REPERENCE: P3330R1C248
CURRENT APPLICATION NUBER: US/10/142,885
CURRENT FILING DATE: 2002-55-10
Prior Apploication removed - See File Wrapper or Palm
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1S-10-158-790-99
Sequence 99, Application US/10158790
Publication No. US20030180879A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                               Sequence 99, Application US/10142885
Publication No. US20030157604A1
GENERAL INFORMATION:
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
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IS-10-142-885-99
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1770 PACABARTABARGTGABATCCCARABABABABABABABABABABABABABABA 1829
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C448
CURRENT APPLICATION NUMBER: 105/10/158, 790
CURRENT APPLICATION NUMBER: 105/10/158, 790
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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT PILING DATE: 2002-05-03
PRIOR APPLICATION TEMOVED - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 99
LENGTH: 1904
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tanabe, Colin K
APPLICANT: Tanabe, Colin K
APPLICANT: Acanabe, Colin K
APPLICANT: Acanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Acanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Acanabe, Colin K
APPLICANT: Wood, William
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING
                                                                                               Sequence 99, Application US/10141756 Publication No. US20030207359A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                          Desnoyers, Luc
Filvaroff, Ellen
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ORGANISM: Homo Sapien
US-10-141-756-99
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330404210N NUMBER: US/10/140,923
CURRENT APPLICATION NUMBER: 2002-05-07
                                                                                                                                                                                                                                                                                                              15 APVAAAATAAAITATAATITTTMVAAAPVAVAAAAAAAAAAASSPATAAATAAAVSPAAA
                                                                                                                                                                         Length 1904;
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                                                                                                                                                                     37.3%; Score 247; DB 15;
53.5%; Pred. No. 1.8e-08;
ilve 7; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 99, Application US/10140923 Publication No. US20030207355A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DeForge. Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Giang
Gerritsen. Mary B.
Goddard, Audrey
Goddwek, Paul J.
Gurney, Austin I.
Sherwood, Steven
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
                                                                                                                                                                     Query Match
Best Local Similarity 53.53
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1890 AAAAAA 1896
; LENGTH: 1904
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-871-99
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75 GOIPAAASVASAAAVAPSAAAAAVQVAPAAPAPVPAPAPIVPVPAPAPAAQASAPAQTQAP 134 74 15 APVARATARAITATARTITTIMVARAPVAVARARARARARARARARARATARARAVSPAAA 0; Gaps Length 1904; Query Match 37.3%; Score 247; DB 15; Length 1 Best Local Similarity 53.5%; Pred. No. 1.8e-08; Matches 68; Conservative 7; Mismatches 52; Indels Search completed: June 16, 2004, 19:17:10 Job time: 14.8105 secs 1890 AAAAAA 1896 135 TSAPAVA 141

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15 APVAAAATAAAITATAATITTIMVAAAPVAVAAAAAPAAAAPSPATAAATAAAVSPAAA 74

0; Gaps

52; Indels

Query Match
37.3%; Score 247; DB 15;
Best Local Similarity 53.5%; Pred. No. 1.8e-08;
Matches 68; Conservative 7; Mismatches 52;

TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-923-99

Length 1904;

1890 AAAAAAA 1896

135 TSAPAVA 141

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75 GOIDAAASVASAAAVAPSAAAAAVQVAPAAAPAPVPAPALVPVPAPAAAQASAPAQTQAP 134

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2M protein - protein search, using sw model

June 16, 2004, 19:09:47; Search time 5.76895 Seconds (without alignments) 2384.384 Million cell updates/sec tun on:

US-09-332-063-4 663 I BSNKTAAVAPISVPAPVAAA......QASAPAQTQAPTSAPAVAPT 143

Title: Serfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 scoring table:

283366 segs, 96191526 residues searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 faximum DB seq length: 2000000000

Ost-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Jatabase :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMARTES

	Description	antifreeze glycope	hypothetical prote	hypothetical prote	polyhydroxyalkanoa	calcium-binding pr	tegument protein 2		cal			7	ж	cyclin-dependent k	regulatory protein	mucin FIM-C.1 - Af	antifreeze glycopr	hypothetical prote	cell wall surface	alginate regulator	hypothetical prote	Ξ		Ę	arylesterase-relat	membrane glycoprot	probable arabinoga	hypothetical prote	phosphoprotein, sy	repetitive protein
SUMMARIES		176	T47182	S29309	G83013	A47282	T42567	SKKLAG	T29018	A47283	T22341	T24591	A35630	G02424	A36128	A45155	A38420	T24592	E95206	G82990	T48814	T35297	VGBEX1	ഹ	83	T45462	55	T33110	4482	011
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	Score	230.5	219.5	218.5	218.5	210	208	207	204.5	204.5	200	196	193	192	189	185.5	183.5	182	182	181	179.5	178	176.5	175	173.5	173	170.5	168.5	167.5	167
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hypothetical prote	clathrin assembly	clathrin assembly	cuticle protein 38	GTP-binding regula	probable multi-dom	core protein homol	immediate-early pr	hypothetical prote	hypothetical prote	high molecular mas	probable iron-sulf	sialidase - Actino	hypothetical prote	zinc finger protei	myc-associated zin
G70555	S36326	536327	UCLQ38	S52418	T50568	T30709	EDBE23	H75253	T15142	T18535	C75259	A49227	H75457	A42170	JC5076
7	7	N	н	N	N	~	Н	N	N	N	N	N	Ŋ	N	N
227 2	896 2	915 2	163 1	846 2	1334 2	421 2	676 1	347 2	418 2	1151 2	1132 2	901 2	395 2	494 2	497 2
25.1 227 2															
	25.1	25.1	25.0	25.0	25.0	24.7	24.7	24.7	24.7	24.6	24.4	24.2	24.1	24.0	24.0

AL IGNMENT'S

RESULT 1 144468 antifreese glycopeptide AFGP polyprotein precursor (imported) - Boreogadus saida antifreese glycopeptide AFGP polyprotein precursor (imported) - Boreogadus saida c;Species: Boreogadus saida c;Species: Boreogadus saida c;Date: 21-Jan-2000 #text_change 21-Jul-2000 c;Accession: T4768 A;Title: Convergent evolution of antifreeze glycopeptides in Antarctic notothenioid A;Recreace numers 122334; MUTD:9756853; PMID:910861 A;Recreace numers 122334; MUTD:9756853; PMID:910861 A;Recreace numers 122334; MUTD:9756853; PMID:910801 A;Recreace numers 123334; MUTD:9756853; PMID:910801 A;Recreace numers 123334; MUTD:9756853; PMID:910801 A;Recreace numers 12334; MUTD:9756853; PMID:910801 A;Recreace numers 12334; MUTD:9756853; PMID:910801 A;Recreace numers 12334; MUTD:9758ARAYTAATAATAATAATAATAATAATAATAATAATAATAATA

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A;Gene: FlyBase:Cpn
A;Cross-references: FlyBase:FBgn0010218
Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology.
C;Keywords: calcium binding
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                                                                                                                                                      159 КТАААКРААКРААКАААКРАА---КРААККТААКТААКРААКРААКРТАКАААКРАТКР 215
                                                                                                                                                                                                                                                                                        216 дакадакраак---радакраакрадаграатдакрадкраякралкралкрая 272
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                                                                                              63
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R,Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1991
A,fitle: Calphotin: a Drosophila photoreceptor cell calcium-binding protein.
A,Reference number: A47282; MUID:93165729; PMID:8094559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: equine herpesvirus 4
A;Variety: strain N880567
C;Accession: T42567
E;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
A;Telte: The DNA sequence of equine herpesvirus-4.
A;Telte: The DNA sequence of equine herpesvirus-4.
A;Reference number: Z22173; MUID:98264497; PMID:9603335
A;Accession: T42567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium-binding protein calphotin - fruit fly (Drosophila melanogaster)
C,Species: Drosophila melanogaster
C,Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
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                                                                                              4 KTAAVAPISVPAPVAAAATAAAITATATITTTMVAAAPVAVAAAAAAAAAAAPSPATAA
                                                                                                                                                                                                                            64 ATAAAVSPAAAGOIPAAASVASAAAVAPSAAAAAAVQVAPAA-PAPVPAPALVPVPAPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: photoreceptor cells
A, Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIP:124956)
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
Pred. No. 1.1e-05;
8; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.7%; Score 210; DB 2;
37.8%; Pred. No. 7e-05;
tive 14; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                              123 AQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                         273 AKPAAPAASSSAPAAPATP 292
45.0%;
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                               63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: A47282
A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-865 <MAR>
   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 PAVAP 200
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AE004091; NID:g9951346; PIDN:AAG08445.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 4 (phaC2 3' region) - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: S29309
R;Timm, A.; Steinbuechel, A.
Bur. J. Biochem. 209, 15-30, 1992
A;Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus A;Reference number: S29303; MUID:93011120; PMID:1396693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAAPAAAAAPSPATAA 63
                                                                                                                                                                 TAAVAPISVPAPVAAAATA-----AAITATATITTTWVAAAPVAVAAAAAPAAAP
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                96 AAAVQVAPA---APAPVPAPALVPVPAPAAQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446 TASVPLAPASASAPAPAPTPVSAPNPAP-----PAPAQTQAQTHKPAQNP 490
                                                                                                     39;
                                      Length 1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 217;
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                   Query Match 33.1%; Score 219.5; DB 2; Best Local Similarity 34.7%; Pred. No. 3e-05; Matches 59; Conservative 25; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 218.5; DB 2
Pred. No. 8.3e-06;
8; Mismatches 62
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A,Experimental source: strain PAO1
C,Genetics:
A,Gene: phaF; PAS060
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A;Molecule type: DNA
A;Residues: 1-217 <TIM>
A;Cross-references: EMBL:X66592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <STO>
                                                                                                                                                                                                                                                                                               58 SP----
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A;Status: pre
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A, Description: The sequence of C. elegans cosmid ZK84
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A,Residues: 1-873 <BAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671 PAPAPAAEST 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 PTSAPAVAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Les 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lermal gland protein APEG precursor - African clawed frog (fragment)
[Species: Xenopus laevis (African clawed frog)
[Species: Anopus laevis (African clawed frog)
[Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jun-2000
[Species: S07498] A34140
[Species: S07498] A34140
[Species: S07498] A34140; Mylo: S0127399; PMID:2298293
                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                       2713 EALLITAPSKPAAAPAPSKPAA-APAPSKPAAPAPSKPAAAPAPSKPAAAPAPSKPAAAP 2771
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2772 APSKPAAPAPASKPAAPPASKPAAPAPSKPAAPPSKPAAPAPAPSKPAAPAPSKPA 2831
                                                                                                                                                                                                                                                                                                                                                                                                             58 SPATAAATAAAVSPAA--AGQIPAAASVAS--AAAVAPSAAAAA----AVQVAPAAPA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 APAPAPAEVEAPAPAPAPAPAPAPAPABGZAPAPARGEAPAPAPABGGZAPAPAPA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --AASVASAAAVAPSAAAAAVQVAPA---APAPVPAP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 GBAPAPARGBAPAPAEGBAPAPAPABGBAPAPAPABGBAPAPAPAPAPAPAPA 273
                                           4;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59539.1; PID:g2605967
4;Experimental source: strain NS80567
                                                                                                                                                                                                                                                                                                      1 BSNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAAPA---AAAAP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZK84.1 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Sate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
3.Kirsten, J.
Submitted to the EMBL Data Library, April 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 APISVPAPVAAAATAAAITATAATITTTMVAAAPVAV.---AAAAAPAAAAPSPATAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A) Residues: 1-416 cRMs-
A) Residues: 1-416 cRMs-
A) Cross-references: EMBL:X51394; NID:g64547; PIDN:CAA35759.1; PID:g1334643
A) Cross-references: EMBL:X51394; NID:g64547; PIDN:CAA35759.1; PID:g1334643
A) Mobile the authors translated the codon TTC for residue 8 as Pro
B) Superfamily: demail gland protein APEG; trefoil homology
B) Rin; tandem repeat
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                     Length 3534;
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                                                                                                                                                                                                                                                     58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2832 AAPAPSKPAAAPASKPAAPAPSKPAAAPAP-SKPAAAP 2870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 PVPA---PALVPVPA-PAAAQA-SAPAQTQAPTSAPAVAP 142
                                                                                                                         i,Note: 24
.;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                                                  Score 208; DB 2;
Pred. No. 0.00027;
8; Mismatches 58
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                                                                                                                                                                                               Query Match
Best Local Similarity 46.2%;
Matches 74; Conservative
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                        1-3534 <TEL>
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A; Molecule type: DNA
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Best Local Simi:
Matches 61;
                                                                                                      ',Genetics:
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C;Species: Drosophila Melanogaster
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: A47283 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: A47283 #sequence_revision K.D.
R;Balinger, D.G; kue, N.; Harshman, K.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993
A;Title: A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and
A;Contents: photoreceptor cells
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A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIP:124959)
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology.
                                                                                                                                                                                                                                                                                 A;Map position: 2
A;Introns: 22/2; 45/3; 108/1
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology.
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                                                                       A,Molecule type: DNA
A,Residues: 1-801 «KTR»
A)Cross-references: EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1
A;Experimental source: strain Bristol N2; clone ZK84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 SAAAVAPSA----AAAAAVQVAPA-----APAPVPAPALVPVPAPAAQASAPAQTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611 ETPAPAPAABETPAPAPAVEETPAPAPAVEETPAPAPAAEETPAPAPAAEVAAEVAEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 801;
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38.9%; Pred. No. 0.00014;
tive 12; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 30.8%; Score 204.5; DB 2; Best Local Similarity 34.7%; Pred. No. 0.00013; Matches 66; Conservative 12; Mismatches 61;
A)Accession: T29018
A)Status: preliminary; translated from GB/EMBL/DDBJ
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Conservative 1
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hypothetical protein F47B8,5 - Caenorhabditis elegans

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Accession: G02424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAVQVAPA-APAPVPAPALVP--V 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 PPAPVMAAPAPLLAPPVPPVAPIVPAFAPRPVLAAPA---FAPALAPAPAFAPAFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AAVAPISVPAPVAAAATA--AAITATAATITTTMVAAAPVA--------VAAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 VAPISVP----APVAAAATAAAITATAATIITTMVAAAPVAV-AAAAAPAAAAAPSP--A 60
                                                                                                                                                                                                                                 4,Cross-references: EMBL:Z77662, PIDN:CAB01192.1; GSPDB:GN00023; CBSP:F47B8.5
4,Experimental source: clone F47B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z70756; PIDN:CAA94793.1; GSPDB:GN00023; CESP:T06E4.7
A;Experimental source: clone T06E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T06E4.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AAPAAAAABSPATAAATAAAVSPAAAGQIPAAASVASAAAAVAPSAAAAAAVQVAPAABAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.6%; Score 196; DB 2; Length 441; Best Local Similarity 42.6%; Pred. No. 0.00024; Matches 63; Conservative 11; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.2%; Score 200; DB 2; Length 581; Best Local Similarity 42.4%; Pred. No. 0.00018; Matches 64; Conservative 7; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                     A;Gene: CESP:F47B8.5
A;Map position: 5
A;Introns: 37/3; 82/3; 122/3; 148/3; 194/1; 217/3; 298/2; 368/1
                                                                                                                                                             4,Status: preliminary; translated from GB/EMBL/DDBJ 4, Wolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-441 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 VPAPALVPVPAPAAQASAPAQTQAPTSAPA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, April 1996
A;Reference number: 219910
A;Accession: T24591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPAAAAAAAAAAIAAITOAP---ISAPAVAP 142
                                          C,Accession: T22341
R,Berks, M.; McMurray, A.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESS:T06E4.7
A;Map position: 5
A;Introns: 104/2; 317/2; 354/3; 404/3
                                                                                                                                                                                                             4, Residues: 1-581 <WIL>
                                                                                                                                         A; Accession: T22341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: T24591
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C. Accession: A35630
R; Kato, J.; Misra, T.K.; Chakrabarty, A.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 2887-2891, 1990
A; Title: a procein resembling eukaryotic histone H1, regulates alginate synthesis A; Reference number: A35630; MUID:90222135; PMID:2109318
                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translecture type: DNA
A;Residues: 1-340 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------AAATAAAVSPAAAGQIPAAASVASAANVAPSAAAAAAVQVAPAA-PA- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 PAAKPVAKPAAKPAAKTAAAKPAAKPAAK---PAAKHVAKPAAKPAAKPAAKPAAKPAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 PRPVAVAVAVSPPLEPAAE-SLDGLEBAPBOLPSVPVPAPASTPPPVPVLAPAPAPAPAPA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 AGQIPAAASVASAAAVAPSAAAAAVQVAPAAPAPAPAPALVPVPAPAAAAAAAASAPAQTQA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- AAPVAVAVIAPAPAPAPAPAPAPAPAPAPAPAPAPA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclin-dependent kinase inhibitor 1C - human
NyAlternate names: cdk-inhibitor 1C; Kip2; p57
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
                                                          C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 KTAAAKPAAKPAAKPAAKPAAKTAAKTAAKPAAKPAAKPVAKPAANAAAKTAAAKPAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KTAAVAPISVPAPVAAAATAAAITA-TAATITTTTWVAAAPVAAAAAAAAAAPSPAT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 193; DB 2; Length 34
Pred. No. 0.00028;
6; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: EMBL:U48869; NID:g1213447; PID:g1213448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PVPA--PALVPVPAPAAQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 KPVAAKPAAAKPATAPAANAAATPSATAAASSAASATP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Residues: 1-316 <REI>
                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M35259
C;Keywords: DNA binding; transcription regulation
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C.Accesion: 002424
R.Reid, L.H.; Weissman, B.E.
submitted to the EMBL Data Library, February 1996
A.Reference number: H01236
   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:CD;KNIC; P57; KIP2
A;Cross=references: GDB:593296; OMIM:600856
A;Map position: 11p15.5-11p15.5
A;Introns: 274/1
protein algR3 - Pseudor
Pseudomonas aeruginosa
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Best Local Similarity 42.4%;
Matches 67; Conservative
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A;Molecule type: DNA
A;Residues: 'MGATTSMRHV' 1-156,'NA',159-173,178-180,'A',182-222,'NA',225-241,'V',243-25
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: isolate cystic fibrosis
A;Note: the authors translated the codon GCC for residue 311 as Ser
A;Note: the authors translated the codon GCC for residue 311 as Ser
Gne 8 4, 31-38, 1989
A;1tle: Nucleotide sequence of a regulatory region controlling alginate synthesis in PB
A;Reference number: JQ0132; MJID:90108714; PMID:2514124
                                                                                                                    R.Deretic, V.; Konyecsni, W.M.

1. Bacteriol. 172, 5544-5554, 1990

2. Bacteriol. 172, 5544-5554, 1990

3.fitle: A procaryotic regulatory factor with a histone H1-like carboxy-terminal domain: A;Reference number: A36128, MUD;91008921; PMID:1698761

A;Reference number: A36128

A;Rotatus: preliminary

A;Rotatus: preliminary

A;Rotatus: preliminary
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1. Biol. Chem. 257, 24620-24624, 1992
A.Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.
A.Reference number: A45155; MUID:93077556; PMID:1447205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVA-PAAPAPVPAPALVPVPAPA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KTAAVAPISVPAPVAAAATAAAITA-TAATITTTWVAAPVAVAAAAAAPAAAABSPATA 62
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    APTTAAAVAATGKOTTAAAEGSAAAEKTAAAGEVSAPPTAAVAATGEDATTAAATAAET 60

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C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
                                                            Date: 30-Nov-1990 #sequence_revision 03-Feb-1994 #text_change 15-Oct-1999
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A; Cross-references: GB: D2115; NID: g214147; PIDN: AAA74725.1; PID: g951460
C; Superfamily: trefoil homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
28.5%; Score 189; DB 2; Length 352;
Best Local Similarity 41.1%; Pred. No. 0.00047;
Matches 58; Conservative 6; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%; Score 185.5; DB 2; Length 40.4%; Pred. No. 0.0012; ive 10; Mismatches 57; Indels
regulatory protein alg? - Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AAATAAAITATAATITTTMVAAAPVAVAAAA---
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F.307-347/Domain: trefoil homology <TRF2>
F.354-394/Domain: trefoil homology <TRF3>
F.526-566/Domain: trefoil homology <TRF4>
F.573-613/Domain: trefoil homology <TRF5>
                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-352 <DER>
A;Cross-references: GB:MS7551; GB:M36050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 AKPAAKPVAAKPAAKPÄTAP 317
                                    Pseudomonas aeruginosa
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                                                                                             Accession: A36128; JQ0148
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Best Local Similarity
Matches 57; Conserv
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71 PAAAGQIP--AAASVASAAAVAPSAAAAAVQVAPAAPAP-----VPAPALVPVPAPA 122
                                                                                61 TAAAGEAPTTTAPATTAAGKAPTTAAATAPTTA-AAGAPTTATGKAPATAAAPVPTTAA 119
                                                                                                                                                                     123 AQASAPAQTQAPTSAPAVAPT 143
                                                                                                                                                                                                                                                 120 SKAPTTAAAATHSTAAAAAPT 140
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Search completed: June 16, 2004, 19:15:40 Job time : 6.76895 secs

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STANDARD;
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SEQUENCE FROM N.A.
STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium-binding.
CONFLICT 36
CONFLICT 43
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Copyright (c) 1993 - 2004 Compugen Ltd.
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NUP1_DROME
SAL3_HUMAN
A180_MOUSE
A180_RAT
CU38_LOCMI
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IFXAD_MOUSE
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Q24742 drosophila Q50360 mycoplasma	P03186 epstein-bar Q9n6k2 drosophila O74352 schizosacch	O9fec4 chlamydomon P45584 locusta mig Q8xrh0 ralstonia s	P08640 saccharomyc P13595 mus musculu	P11675 pseudorabie Q8in94 drosophila
TRX DROVI HMW3 MYCPN	TEGU_EBV OSA_DROSI HOB1_SCHPO	RAA3_CHLRE CU63_LOCMI FTK1_RALSO	AMYH YEAST NCA1 MOUSE	IE18 PRVIF OSA_DROME
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                                                                                                                                                                                                                                                                        Gmachl M., Berger H., Thalhammer J., Kreil G.,
"Dermal glands of Xenopus laevis contain a polypeptide with a highly repetitive amino acid sequence.",
FEBS Lett. 260:145-148(1990).
FIGURION: May act as a growth factor in the germinal layer of the epidermis. May also be involved in growth of regenerating glands and in protection of the skin from the external environment.
-!- SUBCELULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                 aavadisvpapvaaataaaitataati---------tttmvaaapvava--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-25 AND 344-439 FROM N.A. (ISOFORM 2).
MEDLINB-92332564; PubMed=1629230;
Hauber F., Roeben C., Hoffmann W.;
"xP2, a new member of the P-domain peptide family of potential growth factors, is synthesized in Xenopus laevis skin.";
J. Biol. Chem. 267:14451-14455(1992).
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                               XPZ XENLA STANDARD; PRT; 439 AA.

NPT 3. XENLA (208944).
01-7437; Q08944.
01-7406-1990 (Rel. 15, Czeated)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Skin secretozy protein xP2 precursor (APEG protein).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Amphibia: Metacaca; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopodinae; Xenopus.
                                                                                                                                                             48;
                                                                                                                                        Length 865;
                                                                                                                                                            53; Indels
I -> V (IN REP. 2).

p -> A (IN REP. 2).

VQ -> PP (IN REP. 2).

I -> V (IN REP. 2).

S -> T (IN REP. 2).

A -> B (IN REP. 2).

I -> T (IN REP. 2).

A -> B (IN REP. 2).

B -> B (IN REP. 2).

W, 211041780B0077FB CRC64;
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TISSUE SPECIFICITY: Skin.
SIMILARITY: Contains 2 P-type (trefoil) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2,
                                                                                                                                      Score 210; DB 1;
Pred. No. 7.6e-05;
                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1; Synonyms=APEG;
IsoId=P17437-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 3-439 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90127399; PubMed=2298293;
                                                                                                                84781 MW;
                                                                                                                                        31.78;
37.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=2; Synonyms=XP2;
                                                                                                                                                 Local Similarity 37.8 nes 70; Conservative
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703
721
865 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 GEAPAPAPABGEAPAPAPABGEAPAPAPABGEAPAPABGEAPAPABGEAPAPABA
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CAUTION: Ref.2 sequence differs from that shown from position 392 onward and is shorter (418 AA) due to a frameshift.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACID (PROBABLE)
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PYRROLIDONE CARBOXYLIC ACID (PROBABLI
33 X REPEATS OF G-[GE]-[AP] (2,4)-A-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cyclin-dependent kinase inhibitor IC (Cyclin-dependent kinase inhibitor DS7) (p57KIP2).
CDKMIC OR KIP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Indels
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PROSITE; PS00025; P_TREFOLL; 2.
Signal; Growth factor; Alternative splicing; Repeat;
Pyrrolidone carboxylic acid. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 207; DB 1;
Pred. No. 6.6e-05;
8; Mismatches 62
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P-TYPE 2.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 GEAPAPAEGEAPAPAEGEAPAPA 302
                                                                                                                                                                                                                                 EMBL; M90095; AAAS0001.1; -.
EMBL; X51394; CAA35759.1; ALT_FRAME
                                                                                                                                                                                                                                                                            PIR; A37331; A37331.
PIR; S07498; SKXLAG.
HSSP; P04155; 1PS2.
InterPro; IPR000519; P_trefoil.
Pfam; PF00088; trefoil; 2.
PRINTS; PR00680; PTREFOIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41173 MW;
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18
439 AA;
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[1]
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CONFLICT
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18; Gaps

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73

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-----AAPVAVAVLAPAPAPAPAPAPAPAPAPAPAPAPA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AGQIPAAASVASAAAVAPSAAAAAVQVAPAAPAPAPAPALVPVPAPAAQASAPAQTQA
                                                         NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hauser F., Hoffmann W.;
"P-domains as shuffled cysteine-rich modules in integumentary mucin c.i [FIM-C.1) from Xenopus laevis. Polydispersity and genetic polymorphism.";
J. Biol. Chem. 267:24620-24624(1992).
-!- FUNCTION: Could be involved in defense against microbial infections. Protects the epithelia from external environment.
-!- SUBCELDULAR LOCATION: Secreted.
-!- ALFERNATIVE PRODUCTS:
                                                                                                                                                             /FTIG=VAR 001404.
Missing (in heptcocellular carcinomas)
/FTIG=VAR 001405.
Missing (in a bladder cancer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Integrmentary mucin (.1 (FIM-C.1) (Fragment).
Integrmentary mucin (1 (FIM-C.1) (Fragment).
Bukaryota; Metazoa; Chandata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSP_004649, VSP_004650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist. Experimental
confirmation may be lacking for some isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 192; DB 1; Length 316
41.1%; Pred. No. 0.00031;
Live 7; Mismatches 51; Indels
                                                                                                                                                                                                                                                                            /FTId=VAR 001406.
Missing (in a breast cancer)
                                                                                                            /FTId=VSP 000867.
Missing (In several cancers)
                                                                                     (in isoform Short)
P_000867.
                                                                                                                                                                                                                                                                                                                             /FTIG=VAR 001407.
316 AA; 32177 MW; A94CCBF09F8CB3E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=205049-4; Sequence=VSP_004647, VSP_004648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q05049-6; Sequence=VSP_004646, VSP_004648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6 AND 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :sold=Q05049-2; Sequence=VSP_004650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q05049-3; Sequence=VSP_004651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q05049-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Skin;
MEDLINE=93077556; PubMed=1447205;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 41.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 ----PVAAPV----
     209
213
281
11
                                                                                                                                      174
                                                                                                                                                                                            184
                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 PTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 PAPAPAPAP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                   200
                                                                                                                                         171
                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                     VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsucka S., Edwards M.C., Bai C., Parker S., Zhang P., Baldini A.,
Harper J.W., Bledge S.J.,
"PSYMIP2, a structurally distinct member of the p21CIP2 Cdk inhibitor
family, is a candidate tumor suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inford=P49918-2; Sequence=VSP 000867;
-!- TISSUE SPECIFICITY: Expressed in the heart, brain, lung, skeletal muscle, kidney, pancreas and testis. High levels are seen in the placenta while low levels are seen in the liver.
-!- DISEASE: Defects in CDKNIC are involved in tumor formation.
-!- SIMILARITY: Belongs to the CDI family.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Reid L.H., Crider-Miller S.J., West A., Lee M.H., Massague J.,
Weissman B.E.,
                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE OF 12-316 FROM N.A., AND VARIANTS.
MEDLINE=9620999; PubMed=8655143;
TOKINO T., Urano T., Puruhata T., Matsushima M., Miyatsu T., Sasaki S., Nakamura Y.;
                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P49918-1; Sequence=Displayed;
                                                   MEDLINE-95247028; PubMed=7729684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U22398; AAA85095.1; -. EMBL; U48869; AAB05896.1; -. EMBL; D64137; BAA11014.1; -. EMBL; D64137; BAA11015.1; -.
                                                                                                                                                                                         Genes Dev. 9:650-662(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, G02424, G02424.
Genew, HGNC:1786, CDKN1C.
GK, P49918, -.
MIM, 600856; -.
SEQUENCE FROM N.A.
TISSUE=Embryo;
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BY SIMILARITY.
551
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536
DISULPID
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F
              --- FTM: Extensively O-glycosylated.
--- SIMILARITY: Contains 6 P-type (trefoil) domains.

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                                                                                                                                                                         1-8.
P-TYPE 1.
8 X APPROXIMATE TANDEM REPEATS, THR-RICH.
2-1.
2-2.
                                                                                                                                                                                                      8 X 8 AA APPROXIMATE TANDEM REPEATS,
ALA/THR-RICH.
1-1.
1-2.
1-4.
1-5.
1-6.
                                                                 EMBL, 102115; AAA74725.1; -
PIR; ABA74725.1; -
PIR; ABA74725.1; -
PIR; PO1359; AE515.
HSSP; P01359; 2269.
InterPro; IPR00519; P trefoil.
PERNO; PR00680; PTRSPOIL.
SMART; SM00018; PD, 6.
PROSITE; PS00025; P TREFOIL; 6.
Repeat; Glycoprotein; Alternative splicing.
NOW TER 1144 8 X 8 AA APPROXIM
     Isold=Q05049-7; Sequence=VSP_004647; TISSUE SPECIFICITY: Skin.
                                                                                                                                                                                                                                                      250
250
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BY SIMILARITY. BY SIM	28.0%; Score 185.5; DB 1; Length 662; ; Conservative 10; Mismatches 57; Indels 17; Gaps 4; AAATAAAITATAATITITMVAAPVAVAAAAPAAAAAPSPATAAATAAAV 70 APTAAAVAATGEDTTAAAAAAAT 60 PAAAGOIPAAASVASAAAVABVAAAAAAVAVAPAAPVPAPALTAAAAAATITITAAAAAAAAAAAAATTAAAAAAAAAA	စ္တက ပေးဥည္သည္	Glover C. V.C., bldwal A.P., Zdao W.F.; Submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases. [2] GROGENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-Cregon-R; MEDLINE=20196011; PubMed=10731137; MINIARA B., Kafacor E., Vidal S., Brun C., Demailles J., Cadieu E., Papagiannakis G., Spancs L., Louis C., Siden-Kiamos I., Bolsakov S., Meduell J., Peter A., Schoettler P., Werner M., Mourkioti F., Medolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Callister D.M., Campbell L.A., Darlandiscou A., Henderson N.S., MCMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
5531 5599 5999 6100 647 646 646 646 646 629 259 259 278 350 498 415 4174	28.0 40.4 40.4 roative	STANDARD; 1. 34, Creat 1. 35, Last rottin L22, R19J1.4 OR (R0Gaster (F) R0Gaster	Bldwal A.F., 1996) to the l.A. 1; PubMed=107; E.M.K., Ashbu A.S., Lelaure tos F.C., Lour tos F.C., Lour ter A., Schoel e G., Schaefe e G., Schaefe e G., Schaefe
250 573 573 573 573 621 621 641 776 776 776 776 776 776 776 776 776 77	Similarity 40.4%; P. 7; Conservative 10; AAATAAAITATAATITTHWAAATAAAAAGOTPAAASVASAAAYAGGAPTTTAAAGGAPTTTAAAGGAPTTAAAGGAPTTAAAAGGAPTTAAAAAAATT 1	ST2 V3X9; (Rel. 7 (Rel. 33 (Rel. 33 (Rel. 33 (Rel. 4 (Rel. 4 (Rel. 5 (d (CCT-1996) t FEROM N.A. 20196011; Pubm V. Gatt M.K., Gatt M.K., Gloux S., L. Gloux S., L. Fafatos F.C T. Fafatos F.C N., Dowe G., Span J., Peter A., N., Dowe G., San T. D.M., Campbe F.U., Salles
DISOULTD DISOULTD DISOULTD DISOULTD DISOULTD DISOULTD DISOULTD DISOULTD DISOULTD VARSPLIC VAR	Query Match Best Local Si Matches 57; 19 A 1 A 1 A 1 B 1 B 1 A 1 B 1 B 1 B 1 B 1 B 1 B 1 B 1 B 1 B 1 B	DROWE RL22 DROWE P50847; Q9 01-077-195 01-077-195 01-077-206 605 rDosephila RDL22 OR E RDL22 OR E RDL22 OR E RDL22 OR E RDL32 OR E RDL31 OR E R	GLOVET C.V.C., BIG Submitted (OCT-199 [2] SEGUENCE FROM N.A. STRAINE-OFEGON-R; MEDLINE-20196011; MEDLINE-20196011; Barnell B.G., Ferr Dreano S., Gloux S Minana B., Kafatos Papagiannakis G., Modolell J., Pete; Papagiannakis G., Modolell J., Pete; Papagiannakis G., Modolell J., Pete; Modolell J., Secon Modolell J., Secon Modolell J., Secon Modolell J., Secon Modolell J., Secon Modellan P.J., Selective Straines Modellan P.J., Selective Modellan P.J., Select
	\$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	RESULT PERSULT	4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

Notothenia coriiceps neglecta (Black rockcod) (Yellowbelly rockcod) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Meopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomberygii; Percomorpha; Perciformes; Notothenioidei; Nototheniae; Notothenia

SEQUENCE FROM N.A. NCB1_TaxID=8209;

```
Manualide=2019000; PubMed=10731132;
Addams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
Addams M.D., Celniker S.B., Li P.W., Hoskins R.A., Galle R.F.,
Gocoge R.A., Lewis S.B., Zichards S., Asbburner M., Henderson S.N.,
Sutton G.G., Morters J.B., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Fefeffer B.D.,
Amail J.F., Adbayani A., An H.-J., Andrews-Fannkoch C., Baldwin D.,
Ballew R.M., Basen A., Baxendale J., Bardarai D., Bolshakov S.,
Ballew R.M., Basen A., Baxendale J., Bardarai D., Bolshakov S.,
Borkova D., Botchan M.R., Bouch J., Bardranich P., Brotifar P.,
Borton M.R., Bouch J., Baven B.C., Chard J., Bolshakov S.,
Borkova D., Botchan M.R., Bouch J., Bayaktaroglu L., Belshakov S.,
Burtis R.C., Busam D.A., Puller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Deverport L.B., Davies P.,
A Burtis N.C., Brangelista G.C., Ferraz C., Ferriera S., Pletschman W.,
Cober C., Gabrielian A.B., Heinan T.J., Hernardea J.R., Houck J.,
A Hostin D., Houston K.A., Heinand T.J., Wei M.-H., Ibegwan C.,
Julabli M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,
A Hostin D., Houston K.A., Heinand T.J., Wei M.-H., Ibegwan C.,
Julah M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,
Jula Y., Matterei B., Morthosh T.C., McLeed M.P., Moshrefi A.,
Merkulov G., Milshina M.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina M.V., Mobarry C., Morris J., Moshrefi A.,
A Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shan H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Wang Z.-Y., Wassarman D.A., Welley K.C., Web. W. D.,
Willams S.M., Woodsey T., Worley K.C., Web. W.D.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shu M.,
Wang Z.-Y., Wassarman D.A., Zhong W., Zhou X., Zhu X., Smith H.O.,
Spierce Zsyrilber R.A., Morros M., Welley B.C., Siden-Kamos I., Simpson M., Strong R., Shu M.,
Spierce Zsyrilber R.A., Mers R.D., Stang S.,
Schoter Strang
sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                melanogaster.";
Science 287:2220-2222(2000)
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73 AAAKPAAAKPAAASKDAGKKAPAAAAPKKDAKAAAPAPAKAAPAKKAASTPAAAPPAKK 132
                                   --TAAAITATAATITTIMVAAAPVAVAAAAAPA 52
                                                    13 KTAAAKPAEKKAAPAAAAKGKVEKPKAEAAKPAAAAKNVKKASEAAKDVKAAAAAKP 72
                                                                      53 AAAAPSPATAAATA-----AAVSP-----AAAGQIPAAASVASAAAVAPSAA---- 94
                                                                                                                                                                                                                   Antifreeze glycopeptide polyprotein precursor (AFGP polyprotein) (Contains: AFGP7 (AFGP 7); AFGP8 (AFGP 8)] (Fragment).
                   33;
Length 299;
                   Indels
                                                                                                           95 AAAAVOVAPAAPAPVP---APALV-PVPAPAAAQASAPAQ 130
                                                                                                                           133 AAPAKAAPPAAAPAPAAAPAVAKPAPKPKAKAAPAPSK 172
 DB 1;
Score 183.5; DB 1
Pred. No. 0.00084;
9; Mismatches 54
                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                        790 AA
                                                                                                                                                                        PRT;
                                    4 KTAAVAPI-SVPAPVAAAA--
27.7%;
                   64; Conservative
                                                                                                                                                                        STANDARD;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: Antifreeze proteins lower the blood freezing point.
-I- SUBCELLIAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Synthesized by the liver and secreted into the blood from which they become distributed to almost the entire
                                                                                                                                  "An antifreeze glycopeptide gene from the antarctic cod Notothenia coriiceps neglecta encodes a polyprotein of high peptide copy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: Glycosylated; contains disaccharide galactose-N-
acetylgalactosamine attached to threonines in AFGP8 and AFGP7.
-!- DATABASE: NAME=Protein Spotlight;
NOTE=Issue 5 of December 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies of AFGP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://www.expasy.org/spotlight/articles/sptlt005.html"
                                      Hsiao K.-C., Cheng C.-H.C., Fernandes I.B., Detrich H.W. III, Devries A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 87:9265-9269(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extracellular space.
MEDLINE=91067687; PubMed=2251271;
                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO N-TERMINUS AND 457.
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Antifreeze protein; Glycoprotein; Polyprotein; Repeat;

EMBL; M55000; AAA49392.2; -.

A38420; A38420.

X X

30610

SEQUENCE

DOMAIN DOMAIN us-09-332-063-4.rsp

(Alginate regulatory protein

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16-0CT-2001 (Rel. 40, Last annotation update)
Transcriptional regulatory protein algP (Algi
                                                                                                                                                                                                                                                                                         gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 TPATAALNFAATAATPATAATPALIFAATAATAATPATAALNFAATAATAATPATAACNF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 PATAAATAAAVSPA-----AAGQIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TAAVAPISVPAPVAAAATAAA----ITATAATITTIMVAAAPVA--VAAAAAAAAAS 58
           ANTIFREZE GLYCOPEPTIDE POLYPROTEIN.
APGP8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 PAPALVPVPAPAA--AQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 PATAALNFAATAATPATAATPALIFAATAATAATP 338
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Best Local Similarity
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ALGP PSEAB

ID ALGP PSEAB

ID ALGP PSEAE

AC P15276, C9HTU1,

DT 01-APR-1990 (Rel. 14, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                           Deretic V., Konyecsni W.M.;
"A procaryotic regulatory factor with a histone HI-like
"A procarbory-terminal domain: clonal variation of repeats within algP, a
gene involved in regulation of mucoidy in Pseudomonas aeruginosa.";
J. Bacteriol. 172:5544-5554 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Konyecsni W.M., Deretic V.;
"DNA sequence and expression analysis of algp and algo, components "DNA sequence and expression analysis of algp and algo, components the multigene system transcriptionally regulating mucoidy in Pseudomonas aeruginosa: algp contains multiple direct repeats.";
J. Bacteriol. 172:2511-2520(1990).
                                                                                                                                              MEDLINE=90108714; PubMed=2514124; Kato J., Chu L., Kitano K., Devault J.D., Kimbara K., Chakrabarty A.M., Misra T.K.; T.K.; Misra T.K.; R.W.; Misra T.K.; Shucleotide sequence of a regulatory region controlling alginate synthesis in Pseudomonas aeruginosa: characterization of the algR2
                                                               Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                H1, regulates
                                                                                                                                                                                                                                                                                                Kato J., Misra T.K., Chakrabarty A.M.;
"AlgR3, a protein resembling eukaryotic histone H1
alginate synthesis in Pseudomonas aeruginosa.";
Proc. Natl. Acad. Sci. U.S.A. 87:2887-2891(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=PAO / PAO2003;
MEDLINE=90236911; PubMed=2110144;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91008921; PubMed=1698761;
                                                                                                                                                                                                                                                                           STRAIN=8882;
MEDLINE=90222135; PubMed=2109318;
                                                 Pseudomonas aeruginosa.
Bacteria, Proteobacteria; Gamm
Pseudomonadaceae; Pseudomonas.
                                      OR ALGR3 OR PA5253
                                                                                                                                                                                                                                Gene 84:31-38(1989).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                     SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=287;
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us-09-332-063-4.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 AAPSP----ATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 PAAKPVAKPTAKPAAKTAAAKPAAK---PAAKPAAKPAA-KPVAKSAAAKPAAKPAAKPA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KTAAVAPISVP-----APVAAATFAAITATAATITTTWVAABPVAVAABAABAAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. P. R. LIN REF. 1 AND 2).

MISSING (IN REF. 1, 2 AND 3).

A - Y (IN REF. 1, 2 AND 4).

T - A (RIN REF. 1, 2 AND 3).

KP - NA (IN REF. 1, 2 AND 3).

T - A (IN REF. 1, 2 AND 3).

T - A (IN REF. 1, 2 AND 3).

MISSING (IN REF. 1, 2 AND 3).

KP - NA (IN REF. 1, 2 AND 3).

KP - NA (IN REF. 1, 2 AND 3).

KP - NA (IN REF. 1, 2 AND 3).

KP - NA (IN REF. 1, 2 AND 3).

KP - NA (IN REF. 1, 2 AND 3).

KP - NA (IN REF. 1, 2 AND 3).
                                                                                                                                                                 ENBL: A5630; A35630.

PIR: A5530; A35630.

PIR: G82990;

InterPro: IRR06870; PT; 3.

Pfam; PF04886; PT; 3.

Alginate biosynthesis; Transcription regulation; Activator; DNA-binding; Repeat; Complete proteome.

G -> D (IN REF. 4).

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38.3%; Pred. No. 0.0013;
tive 6; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92295S66; PubMed-1318606;
Telford B.A.R., Watson M.S., McBride K., Davison A.J.;
"The DNA sequence of equine herpesvirus-1.";
Virology 189:304-316(1992).
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Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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TO LOEC-1992 (Rel. 24, Created)

TO 1-DEC-1992 (Rel. 24, Last sequence update)

NOTE TO 1-DEC-1992 (Rel. 24, Last sequence update)

NOTE TO 1-DEC-1992 (Rel. 24, Last sequence)

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                            EMBL; M30145; AAA25724.1; -.
EMBL; M35259; AAA25703.1; -.
EMBL; M37551; AAA25703.1; -.
EMBL; M32077; AAA72068.1; -.
EMBL; AE004937; AAG08638.1; -.
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es 59, Conservative
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352 AA;
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RC STRAINSEARCH N.A.

RA SAUGENCE, FROWN N.A.

RA Adman S. Cologoof, PubNed=10731132;

RA Adman S. Cologoof, PubNed=10731132;

RA Adman S. Cologoof, PubNed=10731132;

RA Adman S. Cologoof, S. Cherer S. B., Holf R.A., Boskins R.A., Galle R.F.,

RA Amanatides P. G., Scherer S. B., Holf R.A., Brang O., Chen L.X.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Briton G.G., Worden J. R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Bazesi K.G., Change M., Pfeiffer B.D.,

RA Briton G.G., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktarogul L., Beasley E. M.,

RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,

RA Doddson K., Down L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Doubin K.J., Bvangelista C.C., Ferriaz S., Fleisschmann W.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina M.V., Mobarry C., Morris J., Mosherson D.,

RA Melson D.R., Nol M., Winghy B., Murphy L., Murskern D.R., Paleson D.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 AAAPSPATAAATAAAVSPAA---AGQIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPVP 110
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                                                                                                                                                                                                                                                                                                                                                                                                    2 SNKTAAVAPISVPAPVA-----AAATAAAITATATIT--TTMVAAAPVAVAAAAAPAA
                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                        23;
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable nucleoporin Nup58.
Nup58 OR CG7360.
Drosophia melanogaster (Fruit fly).
Rukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NoBhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                      DB 1; Length 797;
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                                                                                                                                                                                                                                                                      26.6%; Score 176.5; DB 1; Length 30.9%; Pred. No. 0.0041; Live 19; Mismatches 72; Indels
                                                                                         1 22 POTENTIAL.
23 797 GLYCOPROTEIN X.
23 465 SER/THR-R.CH.
766 790 POTENTIAL.
590 S-30 N-LINKED (GLCNAC. .) (PV
797 AA; 80342 MW; 50C9ED9211FSE5B2 CRC64;
                                                                         Signal
EMBL, M86664; AAB02506.1; -. PIR; H36802; VGBKX1.
InterPro, IPR007110; Ig-like.
Glycoprotein; Transmembrane; SIGNAL
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Best Local Similarity 30.99
Matches 51; Conservative
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83 GATSTAAPAFGTAAATPAFGIPAATSAFGAPAATPAFGAAAATPAFGAPAATPAFGAPAA 142

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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

A Shue B.C., Siden-Xiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Yel, Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G.,

A Clabbs R.A., Myers E.W., Rubin G.W., Venter J.C.;

The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE RAD M. Calniker S.E.;

MEDLINE=22426066; PubMed=12537569;

KEDLINE=22426066; PubMed=12537569;

KEDLINE=24260066; PubMed=12537569;

KEDLINE=24260066; PubMed=12537569;

KEDLINE=24260066; PubMed=12837569;

KEDLINE=24260066; PubMed=12837569;

STRAIN-Berkeley; TISSUE=Embryo;

KEDLINE=24260066; PubMed=12837569;

KEDLINE=24260066; PubMed=12837569;

STRAIN-Berkeley; TISSUE=Embryo;

KEDLINE=24260066; PubMed=12837569;

KEDLINE=24260066; PubMed=12837569;

Ceorge R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,

Rubin G.M., Celniker S.E.;

Genome Biol. 3:RESEARCH0080.8(2002).

-I. FUNCTION: Probable component of some nuclear pore complex, a complex sequined for the trafficking across the nuclear membrane complex.
                                                                                                                                                                                                                                                                                                                                                                                        567 MISSING (IN REF. 2).
55528 MW; EBA7C812DDBEEACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004325; Nucleoporin_FG.
Pfam; PF03093; Nucleoporin_FG; 13.
Transport; Nuclear protein; Repeat.
DOMAIN 22 200 17 X2 AA REPEATS OF F-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 175; DB 1;
Pred. No. 0.0037;
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EMBL; AY071440; AAL49062.1; -.
FlyBase; FBGN0038722; Nup58.
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546 AA;
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CONFLICT
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SEQUENCE FROM N.A. (ISOFORM 3). Gooding K., Swoboda K., Molnar M., Gooding K., Angelicheva D., Blechschmidt K., Swoboda K., Molnar M., Tourney I., Kalaydjiewa L.; Ralaydjiewa L.; Resciusion of HSALL3 and refinement of the region for the CCFDN

Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.

gene."

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Homo sapiens (Human)

NCBI_TaxID=9606;

Q9BXĀ9; Q9UGH1; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Sal-like protein 3 (Zinc finger protein SALL3) (hSALL3) SALL3.

1300 AA

STANDARD;

HUMAN

RESULT 10

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SAL3

t

SEQUENCE OF 29-1300 FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=20079154; PubMed=10610715;
Kohlhase J., Hausmann S., Stojmenovic G., Dixkens C., Bink K.,
Schulz-Schaeffer W., Altmann M., Engel W.;
"SALLIZ-Schaeffer W. Altmann M., Engel W.;
"SALLIZ, a new member of the human spalt-like gene family, maps

Genomics 62:216-222(1999).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=4;
Isoid=09BXA9-4; Sequence=VSP_006832;
Isoid=09BXA9-4; Sequence=VSP_006832;
In Sext. Expressed in fetal brain (in neurons of hippocampus,
cortex, mediodorsal and ventrolateral thalamic nuclei, putamen,
cerebellum and brainstem).
DEVENCEMENTAL STAGS: In fetal brain of the 24th gestational week.
SIMILARITY: BELONGS TO THE SAL FAMILY OF C242-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=Q9BXA9-2; Sequence=VSP 006833;
Note=Lacks two zinc finger domains. Major isoform with isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=09BXA9-3; Sequence=VSP 006832, VSP 006833;
Note=Lacks two zinc finger domains. Major isoform with isoform
                                                                                                                                                                                                                                                                                                                                                                                           VARIANT LEU-593, AND REVISIONS TO 787; 797-802; 808; 1138 AND 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Probable transcription factor.
-!- SUBCELLULAR LOCATION: Nuclear (Probable)
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9BXA9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                 Kohlhase J.;
Submitted (JUL-2002) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF347021; AAK18311.1; -. EMBL; AJ007421; CAB65124.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=3;
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9

Gaps

59; Indels 36; Length 546;

9; Mismatches

26.4%; 39.5%;

Query Match
Best Local Similarity 39.5'
Matches 68; Conservative

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---AAAAPSPATAAATAAAVSPAAAGQI--PAAASVASAAAVAPSAAAAAVQV--APAA 105 24 ARPATTTAPPPSFGAATSTP-TFGAAPATTSLFAAPAATPAFGAPAATPAFGAPASTPGF 82 6 AAVAPISVPAPVAAAAITATAAIITITIMVAA-------52

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ID A180_RAT
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                                                                                                                                                                                                                                                                                                                                                                         10 PISVPAPVAAAATAAAITATAATITTTMVAAAPVA-------VAAAAAP---- 51
                                                                                                                                                                                                                                                                                                                              -----AAAAAPSPATAAATAAAVSPAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Clathrin cat assembly protein API80 (Clathrin coat assembly protein API80) (91 kDa synaptosomal-associated protein)
                                                                                                                                                                                                                                                                             76; Gaps
                                                                 protein; Zinc-finger;
                                                                                                                                                                                     (in isoform 2 and isoform 4).
                                                                                                                                                                                           /FIId=VSP 006832.
Missing (in isoform 1 and isoform 2).
/FIId=VSP_006833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukazyota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Buberia, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCSI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=92300439; PubMed=1607933; Zhou S., Sousa R., Tannery N.H., Lafer B.M., Characterization of a novel synapse-specific protein. II. cDNA cloning and sequence analysis of the F1-20 protein.";
                    DB 1; Length 1300;
                                                                                                                                                                                                                                                                             51; Indels
                                                                                                                                                                                                                                    -> C (IN REF. 2).
; 82CF3BDCB6D59150 CRC64;
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                                                                                                                                                                                                                                                                    28.8%; Pred. No. 0.016;
tive 19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          901 AA
                                                                                                                                                                                                                                                             25.3%; Score 168;
                                                                                C242 - TYPE.
C222 - TYPE.
C242 - TYPE.
POLY - GLN.
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                                                                                                                                                                                     Missing
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                                                                                                                                                                                                                                             1300 AA; 135371
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Best Local Similarity 28.8%
Matches 59; Conservative
HSSP, P07248; 1ARE.
Genew, HGNC:10527; SALL3.
MIM; 605079; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                    1044
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Q61548; Q61547;
01-NOV-1997 (Rel.
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VARSPLIC
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DOMAIN
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ID A180 MC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 APATPAPVAAALD-ACSGNDPFAPSEGSARAAPELDLFAMKPPETSAPVVTPTASTAPPV 514
-!- FUNCTION: Adaptins are components of the adaptor complexes which link clathrin to receptors in coated vesicles. Clathrin-associated protein complexes are believed to interact with the cytoplasmic tails of membrane proteins, leading to their selection and concentration. Binding of AP180 to clathrin triskelia induces their assembly into 60-70 nM coats.
-!- SUBCELLULAR LOCATION: Component of the coat surrounding the cytoplasmic face of coated vesicles in the plasma membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 APISVP-APVAAATTAATITATAATITTTWVAAAPVAV----AAAAAAAAAAAPS----
                                                                                                                                                                                                                                                                                                                                                                                                       Name-Stort;
Isodia-60548-2; Sequence=VSP 000172;
Isodia-605548-2; Sequence=VSP 000172;
ISSUS SPECIFICITY: Brain. Associated with the synapses.
-!- DEVELOPMENTAL STRABS: Developmentally regulated in a pattern coincident with active synaptogenesis and synaptic maturation.
-!- DOMAIN: Possesses a three domain structure: the N-terminal 300 residues harbor a clathrin binding site, an acidic middle domain 450 residues, interrupted by an Ala-rich segment, and the C-terminal domain (166 residues).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Phosphorylated. SIMILARITY: Contains 1 epsin N-terminal homology (BNTH) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform Short).
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Coated pits; Alternative splicing; Phosphorylation.
                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2; Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             915 AA
                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q61548-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (:/
/PTId=VSP
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POLY-ALA.
POLY-SER.
POLY-SER.
POLY-SER.
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Conservative
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                                                                                                                                                                                                                                                       FUNCTION: Adoptins are components of the adaptor complexes which rink clathrin to receptors in coated vesicles. Clathrin-associated protein complexes are believed to interact with the cytoplasmic tails of membrane proteins, leading to their selection and concentration. Blunding of AP180 to clathrin triskelia induces their assembly into 60-70 nM coats.
SUBCSILUIAR LOCATION: Component of the coat surrounding the ALTERNATIVE PRODUCTS:
Event-Alternative splicing, Named isoforms=2;
          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-NAR-2004 (Rel. 43, Last annotation update)
16-NAR-2004 (Rel. 43, Last annotation apdate)
17-NAR-2004 (Rel. 43, Last annotation appare)
18-NAR-2004 (Rel. 43, Last ansociated protein API80) (91 kDa synaptoscwal-associated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q05140-2; Sequence=VSP 000173;
DOMAIN: Possesses a three domain structure: the N-terminal 300
residues barbor a clathrin binding site, an acidic middle domain
450 residues, interrupted by an Ala-rich segment, and the C-
                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 epsin N-terminal homology (ENTH) domain.
                                                                                                                                                                                                 Morris S.A., Schroeder S., Plessmann U., Weber K., Ungewickell E., "Clathrin assembly protein AP180: primary structure, domain organization and identification of a clathrin binding site."; EMBO J. 12:667-675(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 166.5; DB 1; Length 915; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32EC1B3BEC5DF8C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMUGL), L.T., -
PROSITE; PS50942; ENTH; 1.
Coated pits; Atternative splicing; Phosphorylation.
                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=005140-1; Sequence=Displayed;
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/FTId=VSP
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POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              terminal domain (166 residues)
                                                                                                                                                                            TISSUE=Brain;
MEDLINE=93178442; PubMed=8440257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X68977; CAA48748.1; -.
EMBL; X68878; CAA48749.1; -.
PIR; S36326; S36326.
InterPro; IPR001026; ENTH.
InterPro; IPR001026; ENTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             915 AA; 93518 MW;
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                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01417; ENTH; 1.
SMART; SM00273; ENTH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                 NCBI_TaxID=10116;
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456 APATPAPVAAALD-ACSGNDPFAPSEGSAEAAPELDL.PAMKPPRISAPVVTPTASTAPPV 514
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-PATAAATAAAVSPAAAGQIPAAASVASAAAV-----APSAAAAAVOVAPAAPAPVPA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 IAAPVGYAAPAVGYAAPA-----IAAAPVAVAHAVAPAAASVANTYRISOTARVLAAP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAAAAAAAAAABSPATAAATAAAVSPA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoejrup P., Andersen S.O., Roepstorff P.; prings structure of a structural protein from the cuticle of the migratory locust, Locusta migratoria."; Biochem. J. 236:713-720(1986).
                                                                                                                                                                                                                                                                                                  20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 04, Last annotation update)
Cuticle protein 38 (LM-18) (LM-ACP 38).
Locusta migratoria (Migratory locust).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea, Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.0%; Score 166; DB 1; Length 16.42.0%; Pred. No. 0.0044; Undels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15320 MW; FBB8C99E2CA66F49 CRC64;
                                                                                                                                    AAAQASAPAQTQAPTSAPAVAP
                                                                                                                                                                         515 PATAPSPAPTAVAATAATTTAAAATTTATTSAAAATTAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protective envelope of other species. SIMILARITY: TO LM-8, LM-67 AND LM-70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86108304; PubMed=3943519;
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                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                        112 PALVPVPAP-
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P04375;
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9 28

Gaps

64;

9; Mismatches

60; Conservative

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SEQUENCE FROM N.A.
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59 AAYAAPAVAAAPAIGYAAPAIAAAPALGYARYAAAAPV-AVAHAAVPAAASVANTYRISQ 117
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90259555; PubMed=8673126;
Mortlock D.P., Post L.C., Innis J.W.;
The molecular basis of hypodactyly (Hd): a deletion in Hoxa 13 leads
The molecular basis of hypodactyly (Hd): a deletion in Hoxa 13 leads
The molecular basis of hypodactyly (Hd): a deletion in Hoxa 13 leads
The molecular basis of hypodactyly (Hd): a deletion in Hoxa 13 leads
Nat. Genet. 13:284-289(1996).

-i-FUNCTION: Sequence-specific transcription factor which is part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Nuclear.
-!- DISEASE: Defects in HOXA13 are the cause of hypodactyly (Hd), a condition characterized by profound deficiency of digital arch
                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.0%; Score 166; DB 1; Length 386; 40.0%; Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 POLY-ALA.
39566 MW; 2B01DCC9B1951324 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structures.
SIMILARITY: Belongs to the Abd-B homeobox family.
                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Homeobox protein Hox-Al3 (Hox-1.10).
                                                                                                                                                             386 AA
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HOMEOBOX.
POLY-GLY.
POLY-ALA.
POLY-ALA.
POLY-ALA.
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PROSITE; PS00071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental
Transcription regulation.
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T03337; -..
MGD; MGI:96173; Hoxa13.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
ProDon; PD00010; Homeobox; 1.
SMART; SM0389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U59322; AAB03322.1; -. HSSP; P14653; 1B72.
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Best Local Similarity 40.0
Matches 56; Conservative
                                 131 TOAPTSAPAVA 141
                                                                 118 TARLLAAPAVA 128
                                                                                                                                                           STANDARD;
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66
84
104
133
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386 AA;
                                                                                                                                                                                                                                                                  HOXA13 OR HOX-1.10
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                         HXAD MOUSE
Q62424;
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DNA BIND
DOMAIN
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                                                                                                                       RESULT 14
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62

Gaps

22;

50; Indels

12; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                            63 AATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAVQVAPAAPAPVPAPAI,VPVPAPAA 122
38 AAAAAAAAAAAAAGGGGFPHPAAAAAGGNFSVAAAAAAAAAAAAAAQCRNLMAHPAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ikeda H., Ishikawa J., Handoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;

Sakaki Y., Hattori M., Omura S.;

"Complete genome sequence and comparative analysis of the industrial microorganism Erreptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003).

-! FUNCTION: One of the essential components for the initiation of protein synthesis. Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30s ribosomal subunits. Also involved in the hydrolysis of GTP during the formation of the 70s ribosomal complex (By similarity).

-! SUBCELLULAR LOCATION: Cytoplasmic.
-! SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=21477403; PubMed=11572948;
MEDLINE=8. I Kedd H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                     15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Translation initiation factor IF-2.
                                                                                                                                                                                                                                                                                              PRT; 1046 AA.
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InterPro; IPR0001787; GTPase_Ras.
InterPro; IPR001787; IF2.
InterPro; IPR002965; P.Ich extensn.
InterPro; IPR001806; Ras trinsfrung.
InterPro; IPR001806; Ras trinsfrung.
InterPro; IPR005225; Small GTP.
InterPro; IPR000000; Translat_factor.
Pfam; PP00009; GTP_EFTU; 1.
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InterPro; IPR001851; Bac inmem transp.
InterPro; IPR004161; BFTU D2.
                                                                                                                                   123 AQASAPAQTQAPTSAPAVAP 142
                                                                                                                                                                              151 KÓCSPCSAAAQSSSGPÁALP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP005031; BAC70262.1; -.
                                                                                                                                                                                                                                                                                              STANDARD;
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Query Match
Best Local Similarity 43.3%; Pred. No. 0.019;
Matches 58; Conservative 4; Mismatches 47; Indels 25; Gaps
                                                                                                          | Prints | Pr04760; IF2_N 2; | | |
| R PRINTS | PR00315; ELONGATNECT. |
| R PRINTS | PR0015 | ELONGATNECT. |
| R PRINTS | PR00449; RASTRNSTRANG. |
| R PROMON | PI186100 | IF2 | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
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| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRO0231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRAMS | TIGR00231; Small Grp | 1. |
| R TIGRO0231; Small G
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF04760; IF2_N: 2.
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69 VSPAAAGQIPAAASVASAAAVAPSAAAAAVQVAPAAAPAVPAPALVPVPAPAAAQASAP 128 9 APISVPAPVAAAATAAAITATAATITTTWVAAAPVAVAAAAAAAAAAAAPSPATAAATAAA 68 g ጽ d ጽ

129 ACTOAPTSABAVAP 142 | || ||| || || |31 EFT-APPSAPA-AP 142

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Search completed: June 16, 2004, 19:17:45 Job time : 4.49633 secs

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09HD27
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Q8vhg2 mus musculu
Q8ndr0 homo sapien
Q96cm5 homo sapien
Q9444 mus musculu
Q81yf3 homo sapien
Q8tbr8 homo sapien
Q8tbr8 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculu
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Q96f99 homo sapien
Q9ukb4 homo sapien
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                                                         (without alignments)
4175.976 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sp208 mns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9qus0 mus
Q8k371 mus
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                                                                                           675
1 MPRAQPSSASYQƏVPADPPA......KIPIQILGQEPDAEMVEYLI
                                                June 16, 2004, 19:17:48 ; Search time 51 Seconds
                                                                                                                                                                             1017041
GenCore version 5,1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                            otal number of hits satisfying chosen parameters:
                                                                                                                                            1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                        ost-processing: Listing first 45 summaries
                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09HD27
08WHG2
08WHG2
08WHG4
09D4H4
09D4H4
08HB8
08HB84
08HB80
08HB80
09HB80
09HB80
09HB80
09HB94
09HB90
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Q8WXD1
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                               sp_unclassified:*
                                                                                                                                                                                                                                                                                                                     sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
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Sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
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sp_human:*
                                                                                                                                                                                                                                         SPTREMBL 25:*
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Q8ten8 homo sapien Q60586 mastowys hi Q80786 pordetella Q7w8G5 bordetella Q7w8G5 bordetella Q7w8G7 bordetella Q7w8G7 bordetella Q7w7F sattus norv Q3xwM7 cryza sattv Q8473 spodoptera Q8673 spodoptera Q8650 sattv Q87414 oryza sattv Q8751 methanosas Q8751 methanosar Q8751 methanosar Q86417 mordetella Q8614 homo sapien Q86414 homo sapien	
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ALIGNMENTS

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SEQUENCE FROM N.A.
MEDLINE-21157403; PubMed=11257124;
Troyanoveky B., Levchenko T., Mansson G., Matvijenko O., Holmgren L.;
"Angiomotin. An angiostatin binding protein that regulates endothelial
Gell migration and tube formation.";
J. Cell Biol. 152:1247-1254 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=99397452; PubMed=10470851;
Kikuno R., Magase T., Ishikawa K., Hirosawa M., Miyajima N.,
Kikuno R., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
Ifor large proteins in vitro.";
DNA Res. 6:197-205(1999).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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EMBL, AB028994; BAA33023.3; -.
Hypothetical protein.
SEQUENCE 675 AA; 72540 WW; BEC28B74427AD481 CRC64;
                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 25, Last annotation update)
Anglomotin (Hypothetical protein KIAA1071).
KIAA1071.
      675 AA
PRT;
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Best Local Similarity 100.
Matches 675; Conservative
      PRELIMINARY;
                                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                                                       457
                                                                                  244 SEYNAAAIMELLREKEERILALEADMIKWEQKYLEENVMRHFALDAAAIVAAQRDTIVIS
                                                                                                                                    398 SEYNAAALMELLREKEERILALEADMIKWEQKYLEENVMRHFALDAAAIVAAQRDTIVIS
                                Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%; Score 24; DB 4; Length 498; D0.0%; Pred. No. 1.3e-12;
                                Indels
                                                                                                                                                                                                304 HSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTLHAQI 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AL833833; CAD38693.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Skin;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014126, AAH1126.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 AA; 35950 MW; 5E28183735E67B56 CRC64;
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                                                                                                                                                                                                                             HSPNTSYDTALEARIOKEBERILMANKRCLDMEGRIKTLHAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to RIXEN CDNA 4932416D09 gene (Fragment).
red. No. 3e-83;
Mismatches 0;
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  Pred. No.
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  ilarity 100.0%; P. Conservative 0;
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Best Local Similarity
Matches 103; Conserv
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TISSUE=Testis;
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SEQUENCE
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                             QRVSBAYENLVKSSSKREALEKAMRNKLEGEIRRMDFNRDLRERLETANKOLAEKEYEG
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                                                                                                          QRVSBAYENLVKSSSKREALEKAMRNKLBGEIRRMHDPNRDLRERLETANKQLAEKEYEG
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  MPRAQPSSASYQPVPADPFAIVSRAQQMVBILSDENRNLRQELSGCYBKVARLQKVETEI
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.3%; Score 103; DB 11; Length 891;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Troyanovsky B., Bratt A., Holmgren L.;
Troyanovsky B., Bratt A., Holmgren L.;
Mhouse angiomotin...;
Submitted (135, AAL73436.1);
MGI:108440; Amot...
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Last annotation update)
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Q8VHG2 Q8VHG2;

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RESULT 2

SEQUENCE Query Match

RESULT 5 2904H4

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256 REKEERILALEADMTKWEOKYLEE 279 671 REKEERILALEADMTKWEQKYLBE 694 PRT; PRT; [1]
SEQUENCE PROM N.A.
STRAIN-CS7BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851; 182 ILALEADMIKWEQKYLEE 199 262 ILALEADMIKWEQKYLEE 279 Best Local Similarity 100. Matches 24; Conservative PRELIMINARY; PRELIMINARY; SEQUENCE FROM N.A. TISSUE=Pancreas; NCBI_TaxID=10090, Query Match Q8BP84 Q8BP84; Q8TBR8; Q8TBR8 RESULT 7 RESULT 8 OSTBRB å Ò STWEET RANK OCC SET THE SO STANDED T SO DE RETERENCE OCCOSORIO DE LA PROPERCIONA DEL PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DEL PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DEL PROPERCIONA DEL PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DEL PROPERCI ઢ PEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CRAIN=CS7BL/6J; TISSUS=Testis;

MEDLINE=21085660; PubMed=11217851;

Arakwa T. Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Arakwa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Adackwa T., Sarawa K., Tzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori P., Bono H., Kasukawa T., Saito R., Asdota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Kadota K., Matsud H.A., Ashburner M., Batalov S., Casavant T., Saito R., Mateso Y., Mikaido I., Pesole G., Quackenbush J., Schriml E., M., Staubli F., Suzuki R., Tomita M., Wagner E., Washio T., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Asakai K., Matsub M., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Asakon M., Satoki M., Satoki K., Wang K.H., Watiz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Arayasahizaki Y., Satokaki Y., Ramasola K., Kawaji H., Kohtsuki S., Trunctional annotation of a full-length mouse cDNA collection.", Red., MGI:19222973; Amocll.

Embr. Akolsofe Bassola M., 88AAFEBSFFAS6046 CRC64;
SeQUENCE 882 AA; 98423 MW; 88AAFEBSFFAS6046 CRC64; ö Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinse, Mus. NCBI_TaxID=10090, Q8IY63;
Q8IX63;
Q1-MAR-2003 (TrEMBirel. 23, Created)
O1-MAR-2003 (TrEMBirel. 23, Last sequence update)
O1-MAR-2003 (TrEMBirel. 23, Last annotation update)
Similar to angiomotin like 1.
Similar to angiomotin like 1.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo. Query Match 3.6%; Score 24; DB 11; Length 882; Best Local Similarity 100.0%; Pred. No. 2.1e-12; Matches 24; Conservative 0; Mismatches 0; Indels SEQUENCE FROM N.A.
TISSUE-Muscle;
Straubberg R.P.
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037539; AAH37539.1; -.
SEQUENCE 956 AA; 106574 MW; 6F47AE3AI3816E95 CRC64; 01-JUN-2001 (TTEMBLrel. 17, Created)
01-JUN-2001 (TTEMBLrel. 17, Last sequence update)
01-OCT-2003 (TTEMBLrel. 25, Last annotation update)
4932416D09Rik protein.
AMOTLI OR 49324-L6D09RIK.
Mus musculus (Mouse) 956 AA. 256 REKERRILALSADMIKWEOKYLER 279 596 REKEERILALEADMIKWEQKYLEE 619 PRT; PRT; PRELIMINARY; PRELIMINARY;

3.6%; Score 24; DB 4; Length 956;

Query Match

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                             Indels
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PIR; PT0534; PT0534.
MGD; MGL1929286; Amotl2.
SEQUENCE 463 AA; 51733 MW; 0394E0334ACFAL7E CRC64;
                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leman colled-coil protein.
100.0%; Pred. No. 2.3e-12; tive 0; Mismatches 0;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Hymos appliens (Human).
Bukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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100.0%; Pred. No. 3.5e-07;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011454; AAH11454.1; ..
Hypothetical protein.
SEQUENCE 466 AA; 51814 MW; AlablaR547CD197C CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MXR-2003 (TrEMBLrel. 23, Last annotation update)
Anglomoctin-like protein 2 variant 1 (Fragment).
Mus musculus (Mouse).
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TISSUE=Brain;
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MEDLINE=22354683; PubMed=12466851;
The PANYOM Consortium,
The PANYOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
The PANYON Consortium,
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
NALLY 420:635-573 (2002).
BMBL; AK040912; BAC30740.1; -.
PIR; PT0534; PT0534.
MGD; MGI:1929286; Amotl2.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"Murine homolog of the human LCCP gene. Variant 2.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF175968; AAD56363.1;
SEQUENCE 463 AA, 51778 MW; 1493D080B4FBBD70 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amotation update)
Angiomotin-like protein 2 variant 2.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 100.0
Matches 18; Conservative
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SECUENCE

Q7TPE4

RESULT 10

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27TPE4

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RESULT 9

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Gaps

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Q96P99 Q96F99;

RESULT 11 Q96F99 TD Q96F9 AC Q96F9 DT 01-DE

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IISSUE=Brain;

MEDLINE=99246063; PubMed=10231032;

MEDLINE=99246063; PubMed=10231032;

Magaze T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,

Majajiama N., Tanaka A., Kotani H., Nomura N., Ohara O.,

"Prediction of the coding sequences of unidentified human genes. XIII.

The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";

EMBL; AB021306; BAA76833.1; -.
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QBC371;
O1-OCT-2002 (TERMBLrel. 22, Last sequence update)
O1-OCT-2003 (TERMBLrel. 25, Last sequence update)
O1-OCT-2003 (TERMBLrel. 25, Last annotation update)
Similar to angiomotin like 2.
AMOTIL:
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmaalia; Etheria: Rodentia; Sciurognathi; Muridae; Musinae; Musculus interpretations.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KlAA0989 (Fragment).
KLAA0989.
Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SESTING STRUNG OF THE human LCCP gene. Variant 1.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF175967; AAD56362.2; -.

EMBL; AF175967; AAD56362.2; -.

EMDJ; AF1759586; Amotl2.

NON TER 1

SEQUENCE 586 AA, 64946 MW; 4103EBA23B7CE613 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC0278214 AAH27824.1; -. MGD; MGIL 1229286; Amocll 2. SEQUENCE 772 AA; 85278 MW; 9979F5F4D2A54989 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            772 AA
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01-NOV-1999 (TrEMBLrel. 12, Created)
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SEQUENCE FROM N.A.
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Gaps
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2.7%; Score 18; DB 4; Length 859;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
Genew; HGNC:17812; AMOTLZ.
InterPro; IPR000408; Reg_chr_condens.
PROSITE; PS00626; RCC1_2; 1.
Hypothetical protein.
1 1 1 1 SEQÜENCE 859 AA; 94325 MW; 5AP7E211E4CF738D CRC64;
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12434, Ap
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Patent No. 5482709
Sequence 6784, Ap
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10, Appl
10, Appl
                                                                   June 16, 2004, 19:25:49; Search time 23 Seconds (without alignments) 1515:110 Million cell updates/sec
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Sequence 5, Appli
Sequence 5, Appli
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Patent No. 9
Sequence 40
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1. /cgr2 = //ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2 = f/ptodata/2/iaa/5B_COMB.pep:*

3. /cgn2 = f/ptodata/2/iaa/6A_COMB.pep:*

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5. /cgn2 = f/ptodata/2/iaa/PcTUS_COMB.pep:*

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5. /cgn2 = f/ptodata/2/iaa/PcTUS_COMB.pep:*

5. /cgn2 = f/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-434-418-2
US-08-433-288-2
US-08-174-739A-2
US-08-903-814A-2
US-09-903-814A-2
US-09-489-039A-12434
US-08-494A-2
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US-09-050-739-64
US-08-074-12L-5
PCT-US94-06447-5
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-09-252-991A-28326
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US-09-252-991A-24427
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-09-968-927-10
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                                               M protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Match Length DB
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No.
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17, Appl	153, App	153, App	8, Appli	23, Appl	23, Appl	6, Appli	2, Appli	43, Appl	43, Appl	43, Appl	43, Appl	13, Appl	13, Appl	33, Appl	33, Appl	36, Appl	36, Appl
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence
US-09-326-203A-17	US-09-688-188B-153	US-09-291-417D-153	US-08-042-747A-8	US-08-804-439A-23	US-08-720-229-23	US-09-150-460B-6	US-08-826-267-2	US-08-433-854-43	US-08-174-745A-43	US-08-195-947-43	US-08-433-885-43	US-08-433-908B-43	US-08-410-614-43	US-07-814-220-33	US-07-812-421-33	US-07-814-220-36	US-07-812-421-36
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ALIGNMENTS

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Patenn No. 5273901
PAPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON, 19025MD. 1:000-92. SHARNON M.; STRAUSBERG, SUDAN L.;RUPP,WICCHAIL D.;
AUGUSTINE, PATRACTAC, 1,DANFORTH, HARRY D.
PATENTAC PROPERTION DATA:
CURRENT APPLICATION DATA:
PRINCE DATE: S. M. ANTICHEN, AC-6B
PRILING DATE: 1.5 SEP-1990
PRILING DATE: 1.5
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500 AAAVAVAAA 509
               40 AAAPVAVAAA 49
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18-09-107-532A-6784
Sequence 6784, Application US/09107532A
Sequence 6784, Application US/09107532A
Patent No. 65837A
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION:
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                  1.6%; Score 11; DB 6; Length 76; 100.0%; Pred. No. 0.017; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COM
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LOCATION: (B) LOCATION 1...127
SEQUENCE DESCRIPTION: SEQ ID NO: 6784:
IS-09-107-532A-6784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 11; Conservative
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500 AAAPVAVAAA 509

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                                                                                        GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OFTINGER, Thomas
APPLICANT: RESURESEN, Peter
APPLICANT: RASMINGEN, Malter
APPLICANT: RASMINGEN, Malter
APPLICANT: FLORIO, Walter
APPLICANT: FLORIO, Walter
APPLICANT: FLORIO, Walter
APPLICANT: FLORION: NUCLEIC ACIDS FRACKENTS AND POLYPEPTIDE FRACKENTS
TITLE OF INVENTION: DERLYED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERLYED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICANTON NUMBER: 0376/97
EARLIER FILING DATE: 1998-03-03
EARLIER APPLICANTON NUMBER: 1277/97
EARLIER APPLICANTON NUMBER: 60/044,624
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PATENTING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 64
LENTH: 130
TYPE: PRT

CORGANISM: Mycobacterium tuberculosis
US-09-050-739-64
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1 Sequence 5, Application US/08074121
1 Facent No. 576736
2 GENERAL INFORMATION:
APPLICANT: Best, Elaine
APPLICANT: Rest, Elaine
APPLICANT: Convertion: Lipid Content of Plant Tissues
ITILE OP INVENTION: Richardson
STREET: 2000 Sand Hill Road, Suite 100
CITY: Menlu Type: Ploppy disk
COUNTER: Elb PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/074,i21
FILING DATE: 08-UNN-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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S-09-050-739-64
Sequence 64, Application US/09050739
Patent No. 6641814
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Sequence 27059, Application US/09252991A
| Sequence 27059, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al. |
| APPLICANT: Marc J. Rubenfield et al. |
| TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: WIGHER: US/09/252,991A |
| CURRENT APPLICATION NUMBER: US/09/252,991A |
| CURRENT PILING DATE: 1999-02-18 |
| PRIOR APPLICATION NUMBER: US/07/4,788 |
| PRIOR APPLICATION NUMBER: US/07/4,190 |
| PRIOR PILING DATE: 1998-02-18 |
| PRIOR PILING DATE: 1998-07-27 |
| NUMBER OF SEQ ID NOS: 33142 |
| SEQ ID NOS: 33142 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILLSON,
SUSSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN I.;RUFF,MICHAEL D.;
AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
;SPOROZOITE 21.5 KB ANTIGEN, AC-6B
NUMBER OF EXCURSES: 11
CURRENT APPLICATION DATA:
FILING DATE: 12-SEP-1990
PRIOR APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 215,162
FILING DATE: 19-JUL-1988
PRIOR APPLICATION NUMBER: 25,701
FILING DATE: 19-JUL-1988
PRILING DATE: 19-JUL-1988
PRILING DATE: 19-JUL-1988
PRILING DATE: 19-JUL-1988
PRILING DATE: 19-JUL-1984
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APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON, SUSAN D.;POFE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.;
AUGUSTIANE, PATRICIA C.;DANFORTH, HARRY D.
TITLE OF INVENTION: RIMERIA ANTIGENIC COMPOSITION WHICH SHLICITS ANTIEODIES AGAINST AVIAN COCCIDIOSIS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 4; Length 170;
Pred. No. 0.31;
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Pred. No. 0.33;
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100.0%; Pred. No. .
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.5
Best Local Similarity 100.
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5273901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application PC/TUS9406447
GENERAL INFORMATION:
APPLICANT: Calgene, Inc.
TITLE OF INVENTION: Methods and Compositions for Modulating
TITLE OF INVENTION: Lipid Content of Plant Tissues
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Well, Gotshal & Manges
STREET: 2882 Sand Hill Road, Suite 280
CITY: Meanlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                            Score 10; DB 1; Length 156;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5%; Score 10; DB S; Length 156;
100.0%; Pred. No. 0.28;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06447
FILING DATE: 06-JUN-1994
CLASSIPICATION:
REGISTRATION NUMBER: 32,750
REPERBENCY DOCKET NUMBER: 05938/043001
TELEPHONE: (415) 854-5277
TELEPHONE: (415) 854-6277
TELERAX: 200154
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                         Query Match
1.5%; Score 10; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Rea-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE-097/WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEPHAX: (415) 854-3713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TOPOLOGY: 11-7
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Matches 10; Conservative
                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-074-121-5
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CT-US94-06447-5
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Pred. No. 0.54; 0; Mismatches

521 ATAAATAAAV 530

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Best Local Similarity 100.0%;
Matches 10; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Sinth, Penelope
APPLICANT: Swith, Penelope
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Therry
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6180368ris
STREET: 1 Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                  1.5%; Score 10; DB 6; Length 180; 100.0%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                               0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/413,974
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REPRENCE/DOCKET NUMBER: IMPH-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPRAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: US/07/746,703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-413-974-2

) Sequence 2, Application US/08413974

) Patent No. 6180368

) GENERAL INFORMATION:
PILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 581,693
PILING DATE: 12-5EP-1990
APPLICATION NUMBER: 215,162
PILING DATE: 05-UUL-1985
APPLICATION NUMBER: 746,520
FILING DATE: 19-UTN-1985
APPLICATION NUMBER: 627,811
PILING DATE: 05-UUL-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
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1.5%; Score 10; DB 3; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels
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WESULT 12
WESULT 12
Sequence 2, Application US/08433288
| Patent No. 6292698
| GENERAL INFORMATION:
| APPLICANT: Singh, Mohan Bir et al. |
| TITLE OF INVENTION: REGRESS POLLEN ALLERGEN FILE REFERENCE: IM-051CWD1
| CURRENT APPLICATION: NUMBER: US/08/433,288
| CURRENT APPLICATION NUMBER: US/08/433,288
| PRIOR APPLICATION NUMBER: US/08/13,947
| PRIOR FILING DATE: 1994-03.30
| PRIOR FILING DATE: 1994-02-25
| PRIOR FILING DATE: 1994-02-26
| PRIOR FILING DATE: 1991-08-16
| PRIOR FILING DATE: 1991-08-1
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SINGh, Mohan Bir et al.
TITLE OF INVENTION: RYERRASS POLLEN ALLERGEN
FILE REPERENCE: IMT-051CND2
CURRENT APPLICATION NUMBER: US/08/434,418
CURRENT APPLICATION NUMBER: US/08/434,418
CURRENT APPLICATION NUMBER: 1995-05-03
PRIOR APPLICATION NUMBER: 09/202,861
PRIOR PILING DATE: 1994-25-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 308
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100.0%; Pred. No. 0.54;
tive 0; Mismatches 0
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Patent No. 6197313
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Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Lolium perenne
US-08-434-418-2
281 ATAATAAAV 290
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RESULT 13

Length 308;

DB 3;

1.5%; Score 10;

Query Match

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RESULT 15
US-09-903-814A-2
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APPLICANT: Singh, Mohan Bir, Knox, Robert B., Smith, Penelope,
APPLICANT: Aryioglu, Asil, Theerakulpisut, Piyada, Hough, Terryn
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6451324Tis
STREET: 1 Liberty Place, 46th Ploor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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100.0%; Pred. No. 0.54;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,739A
FILING DATE: 29-DEC-1993
CLASSIFICATION: 435
ATYORNEX/ACENT INFORMATION:
NAME: MAIGH AND STORM RECEIVED TO TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 227-7400
TELEPAX: (617) 227-5941
INPORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19103
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                 APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Poeet B
APPLICANT: Singh, Peneloge
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Googly, Asil
APPLICANT: Googly, Terryn
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Lahive & Cockfield, LLP
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
                      Sequence 2, Application US/08174739A
Patent No. 6265566
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESULT 14
S-08-434-256-2
Sequence 2, Application US/08434256
Patent No. 6451324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 308 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
S-08-174-739A-2
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S-08-174-739A-2
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100.0%; Pred. No. 0.66;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09903814A

Patent No. 6680428

GENERAL INFORMATION:
APPLICANT: Rancou, Layo O.
APPLICANT: Pancou, Layo O.
APPLICANT: Alalski, Antoni
APPLICANT: Aralski, Antoni
APPLICANT: Thorpe, Cathy
TITLE OF INVENTION: Tetrahydrofolate Metabolism Enzymes
FILE REFERENCE: BB1179 USDIV
CURRENT APPLICATION NUMBER: US 60/092,869
FILE REFERENCE: B1179 USDIV
CURRENT APPLICATION NUMBER: US 60/092,869
FRIOR FILING DATE: 1998-07-15
FRIOR FILING DATE: 1998-07-15
FRIOR FILING DATE: 1998-07-15
FRIOR FILING DATE: 1998-07-12
SRIOR FILING DATE: 1998-07-12
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/434,256
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: 33,712
REFERENCE/DOCKET NUMBER: 1MPH-0003
TELECHMONICATION INFORMATION:
TELEPHONE: (215)568-3949
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-434-256-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 16, 2004, 19:31:43 Job time : 24 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.5
Best Local Similarity 100.
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 ATAATAAAV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 ATAATAAN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 VPAPVAAAAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 VPAPVAAAT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
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us-09-332-063-2.oli.rapb

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Sequence 36456, A Sequence 3389, A Sequence 87, Appl Sequence 2, Appli Sequence 65, Appli Sequence 605, Appl Sequence 13871, A Sequence 13871, A Sequence 1360, Appl S
                                                                                                                                                                                                                June 16, 2004, 19:27:24 , Search time 49 Seconds (without alignments) 3880.921 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                       US-09-332-063-2
675
1 WFRAQPSSASYQPVPADPFA......KTPIQILGQEPDAEXVBYLI 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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2: /cgn2_6/ptodata/2/pubpaa/USO7_REW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1158786
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-864-761-36456
US-09-864-761-33389
US-09-864-761-33389
US-10-204-887-87
4 US-10-298-417-2
5 US-10-298-417-2
5 US-10-298-417-2
5 US-10-298-417-4
2 US-10-369-431-3871
5 US-10-369-493-3871
5 US-10-369-493-3424
2 US-10-369-493-3424
6 US-10-389-566-1360
6 US-10-389-566-1360
6 US-10-389-566-1365
US-10-389-566-1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1158786 segs, 281726120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ost-processing: Listing first 45 summaries
                                                                                                                                              M protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inimum DB seq length: 0 aximum DB seq length: 2000000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                   itle:
erfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coring table:
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Sequence 13588, A Sequence 5,450, A Sequence 20, Appli Sequence 1441, Appli Sequence 1737, Appli Sequence 1314, Appli Sequence 1314, Appli Sequence 1314, Appli Sequence 1316, Appli Sequence 170, Appli Sequence 6, Appli Sequence 1286, Appli Sequence 1794, Appli Sequence 17944, Appli Sequence 17944, Appli Sequence 179444, Appli Sequence 17
              2 US-10-282-122A-57450

5 US-10-386-050A-6

6 US-10-389-566-1441

6 US-10-389-566-1863

6 US-10-389-566-1863

6 US-10-389-566-1837

6 US-10-389-566-1314

6 US-10-389-566-1314

6 US-10-389-566-1315

10-10-389-566-1315

10-10-389-566-1315

10-10-389-566-1315

10-10-389-566-1315

10-10-389-566-1315

10-10-389-566-1315

10-282-122A-62378

2 US-10-282-122A-62378

2 US-10-282-122A-6443

2 US-10-282-122A-6443

2 US-10-389-566-1286

1 US-10-389-566-1368

1 US-10-389-566-1368

1 US-10-389-566-1368

1 US-10-389-566-1368
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ALIGNMENTS

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RESULT 1
US-09-864-761-36456
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us-09-332-063-2.011.rapb

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RESULT 3
US-09-864-761-43939
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US-09-864-761-39389

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US-09-864-761-39389

US-08-864-761-39389

US-08-864-761-39389

US-08-864-761-39389

US-08-864-761-39389

US-08-864-761-39389

APPLICANT: Penn, Sharron G. APPLICANT: Hanzel, David R. APPLICANT: Chen, Wencheng K. APPLICANT: Chen, Wencheng CRNME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL POR TITLE OF INVENTION: HUANA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL POR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REPEBENCS: Acomica-X-1 US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-06-03

PRIOR PILING DATE: 2000-06-04

PRIOR PILING DATE: 2000-06-04

PRIOR PILING DATE: 2000-06-04

PRIOR PILING DATE: 2000-06-07

PRIOR PILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 MPRAQPSSASYQPVPADPPAIVSRAQQMVEILSDENRNLRQELEGCYEKVARLQK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPRAQPSSASYQPVPADPFAIVSRAQQMVBILSDENRNLRQBLEGCYBKVARLQK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRI
ORGANISM: Homo sapiens
FERTURE: PRORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN PEACENNE, S.6
OTHER INFORMATION: EXPRESSED IN PEACENNE, S.6
OTHER INFORMATION: EXPRESSED IN MAULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.1%; Score 55; DB 9; Length 208; Best Local Similarity 100.0%; Pred. No. 1e-39; Matches 55; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 36456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRI
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 7.5
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 9.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.0
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.0
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.00e-20.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VETEIQRVSEAYEMLVKSSSKREALEKAMRNKLEGEIRRWHDFNRDLR
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7.1%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.7e-34;
Matches 48; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49117
SEQ ID NOS: 49389
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APPLICANT: ROSBBERRY, Ann M.
APPLICANT: ROSBBERRY, Ann M.
APPLICANT: ROSBBERRY, Ann M.
APPLICANT: ROSSO, Frank D.
APPLICANT: STORSO, Frank D.
APPLICANT: STORSO, Frank D.
APPLICANT: MISSO, Frank D.
APPLICANT: MISSO, Frank D.
APPLICANT: MISSO, Frank D.
APPLICANT: WISSO, Frank D.
APPLICANT: WISSO, Frank D.
APPLICANT: STORE D.
APPLICANT: STORE D.
APPLICANT: GIBM M.
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-229-41/-2

US-10-229-41/-2

Sequence 2, Application US/1028417

Publication No. US20030124603A1

GENERAL INPORMATION:

APPLICANT: Mayuki Nishimura

APPLICANT: Mayuki Nishimura

APPLICANT: Witchi Ono

APPLICANT: Work Inno

APPLICANT: York Inno

APPLICANT: Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030124569Al LI:212029.1.orf2:2000FEB01
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3.6%; Score 24; DB 14; I
Best Local Similarity 100.0%; Pred. No. 4.2e-12;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 REKBERILALEADMTKWBQKYLEB 346
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NAME/KEY: unsure
LOCATION: 18, 388
COTHER INFORMATION: unknown or other
US-10-204-887-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
US-10-298-417-2
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US-10-298-417-2
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OTHER INFORMATION: BERFESSED IN ADULT LIVER, SIGNAL = 0.56
OTHER INFORMATION: BERFESSED IN PLACENTA, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.9%; Score 26; DB 9; Length 26; Best Local Similarity 100.0%; Pred. No. 4.1e-15; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
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Sequence 87, Application US/10204887
Sequence 87, Application US/10204887
Publication No. US2003012456941
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SPIRO, Peter A.
APPLICANT: SFIRO, Peter C.
APPLICANT: SFIRO, Peter C.
APPLICANT: GENOMICA, Steven C.
APPLICANT: GENOMICA, Simon C.
APPLICANT: CHEN, Alice
APPLICANT: CHEN, Alice
APPLICANT: DAMIELS, Stefan.
APPLICANT: DAMIELS, Stefan.
APPLICANT: DAMIELS, SUBAN C.
APPLICANT: DAMIELS, SUBAN E.
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GREENAWALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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APPLICANT:
APPLICANT:
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ô Query Match 2.7%; Score 18; DB 14; Length 772; Best Local Similarity 100.0%; Pred. No. 9.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels

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APPLICANT: Tang, V. Tom
APPLICANT: Tang, Yongbong
APPLICANT: Tang, Yongbong
APPLICANT: Tang, Yongbong
APPLICANT: Weng, Zhiwei
APPLICANT: Weng, Cachi
TITLE OF INVENTION: Polypeptides
FILE OF INVENTION: POLYPER: US 00/09-13
FRIOR APPLICATION NUMBER: US 09/488,725
FRIOR FILING DATE: 2000-01-21
FRIOR FILING DATE: 2000-04-25
FRIOR APPLICATION NUMBER: PCT/US01/02623
FRIOR APPLICATION NUMBER: US 09/499,404
FRIOR FILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: US 09/496,914
FRIOR FILING DATE: 2000-02-03
FRIOR APPLICATION NUMBER: US 09/496,914
FRIOR FILING DATE: 2000-02-03
FRIOR FILING DATE: 2000-03-03
FRIOR APPLICATION NUMBER: US 09/496,914
FRIOR FILING DATE: 2000-03-03
FRIOR FIL Sequence 605, Application US/10243552 Publication No. US20030224379A1 GENERAL INFORMATION:

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Query Match 2.7%; Score 18; DB 15; Length 467; Best Local Similarity 100.0%; Pred. No. 6e-07; Matches 18; Conservative 0; Mismatches 0; Indels

TYPE: PRT CRCANISM: Homo sapiens JS-10-094-466-52

⋧

JS-10-298-417-4

Query Match 1.6%; Score 11; DB 12; Length 22 Best Local Similarity 100.0%; Pred. No. 0.43; Matches 11; Conservative 0; Mismatches 0; Indels CRGANISM: Homo sapiens US-10-243-552-605

Sequence 4, Application US/10298417
Publication No. US20030124603A1
GENERAL INFORMATION:
APPLICANT: Mayumi Asano
APPLICANT: Mayumi Asano
APPLICANT: Wuichi Ono
APPLICANT: Yorko Inoue
APPLICANT: Yoko Inai

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Gaps

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Length 228;

507 AAAAAAAAA 517

GENERAL INFORMATION:

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Query Match 1.6%; Score 11; DB 15;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 11; Conservative 0; Mismatches 0
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Sequence 10023, Application US/10369493
Sequence 10023, Application US/10369493
Publication No. US20030233675A1
GENERAL IRPORANTION:
APPLICANT: Go. Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES
FILE REPRENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10023
LERGHH: 443
TURNEY OF THE WARRENT OF TH
UESULT 9
15-10-569-493-13871

Sequence 13871, Application US/10369493

Publication No. US2003023675A1

Publication No. US2003023675A1

Publication No. US2003023675A1

APPLICANT: Cao, Yongwei

APPLICANT: Gaidman, Barry

APPLICANT: Glader, Steven C.

APPLICANT: Glader, Marie Natury

APPLICANT: Glader, Marie Natury

APPLICANT: Glader, Marie Natury

APPLICANT: Glader, William Coldman, WILL OF INVENTION: PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

RUMBER OF SEQ ID NOS: 47374

SEQ ID NO 13871

LENGTH: 407

TYPE: PRT

CRCANISM: Pseudomonas fluorescens

US-10-369-493-13871
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1.6%; Score 11; DB 15; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 11; DB 15; Length 407; 106.0%; Pred. No. 0.73; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESULT 11
18-10-369-493-3424
18-10-40-ence 3424, Application US/10369493
Publication No. US20030233675A1
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Matches 11; Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Galdman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE DF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS POR PRODUCTION OF
ITILE DF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US 60/360,039
FRIOR PILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
FRIOR PILING DATE: 2002-02-21
NUMBER OF ESO ID NOS: 47374
SEQ ID NO 3424
ILENGTH: 1906
TYPE: PRT
ORGANISM: Neurospora crassa
FRATURE:
NUMBER (1): (1906)
CATION: (1): (1906)
CATION: (1): (1906)
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| Sequence 60991, Application US/10282122A
| Sequence 60991, Application US/10282122A
| Sequence 60991, Application US/10282122A
| Sequence 60991, Application US/10282122A
| SEREAL INFORMATION: Zamudo, Carlos
| APPLICANT: Zamudo, Carlos
| APPLICANT: Wall, Daniel
| APPLICANT: Wall, Daniel
| APPLICANT: Wall, Daniel
| APPLICANT: Wall, Daniel
| APPLICANT: Trawick, John
| APPLICANT: Tocsych, R.
| TITLE OF INVENTION INDERS: 2003-220
| CURRENT APPLICANTON NUMBER: 60/220, 335
| PRIOR FILING DATE: 2000-05-26
| PRIOR PLICATION NUMBER: 60/220, 335
| PRIOR PLICATION NUMBER: 60/260, 336
| PRIOR PLICATION N
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us-09-332-063-2.oli.rapb

DB 16; 'Length 120; 1.8;

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Query Match 1.5%; Score 10; DB Best Local Similarity 100.0%; Pred, No. 1.8 Matches 10; Conservative 0; Mismatches
                               ; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-389-566-1545
                                                                                                                                                                                                                              500 AAAPVAVAAA 509
       ·LENGTH: 120
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JS-10-389-566-1360

JS-10-389-566-1360

Publication No. UB200040025202A1

GENERAL INFORMATION:

APPLICANT: Monsanto Technology, LiC

APPLICANT: Monsanto Technology, LiC

TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants:

TITLE OF INVENTION: NUMBER: US/10/389,566

CURRENT APPLICATION NUMBER: US 60/365,301

PRIOR APPLICATION NUMBER: US 60/365,301

PRIOR APPLICATION NUMBER: US 60/365,301

PRIOR APPLICATION NUMBER: US 60/391,786

PRIOR PILING DATE: 2002-06-25

PRIOR PILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SOFTWARE: PATENT OF NOS: 2459

SOFTWARE: PATENT OF NOS: 2459

SOFTWARE: PATENT OF NOS: 2459

SOFTWARE: LICO
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Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICAMT: Monator Technology, LLC
APPLICAMT: Monator Technology, LLC
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants:
FILE REPERBNCE: 38-77(52900) D
CURRENT FILING DATE: 2003-03-15
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SEQ ID NO 1545
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM,
NUMBER OF SEQ ID NOS: 78614
SCPTWARE: PatentIn version 3.1
SEQ ID NO 60991
LENGTH: 120
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1.8;
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1.8;
                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                   Query Match 1.5%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.5%; Score 10;
Best Local Similarity 100.0%; Pred. No.
Matches 10; Conservative 0; Mismatch
                                                                                                                                                                         ORGANISM: Listeria monocytogenes
US-10-282-122A-60991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Listeria innocua
JS-10-389-566-1360
                                                                                                                                                                                                                                                                                                                                                     500 AAAPVAVAAA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 AAAPVAVAAA 509
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haseleeck, Kobert
APPLICANT: Oblean, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Xu, H Howard
ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Herokaryotes
FILE REPERRY: Xu, H HOWARD
ITILE OF INVENTION: Jentification of Essential Genes in TITLE OF INVENTION: 1000-03-21
FRIOR REPLICATION NUMBER: 60/191,078
FRIOR PELICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-25
FRIOR PELICATION NUMBER: 60/206,848
FRIOR PELICATION NUMBER: 60/206,930
FRIOR PELICATION NUMBER: 60/205,625
FRIOR PELICATION NUMBER: 60/205,625
FRIOR PELICATION NUMBER: 60/205,931
FRIOR APPLICATION NUMBER: 60/205,931
FRIOR PELICATION NUMBER: 60/205,931
FRIOR PELICATION NUMBER: 60/205,931
FRIOR PELICATION NUMBER: 60/205,308
FRIOR FILING DATE: 2000-11-27
FRIOR PELICATION NUMBER: 60/205,931
FRIOR PELICATION NUMBER: 60/205,931
FRIOR FILING DATE: 2001-02-16
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Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 10; Conservative 0; Mismatches 0
                                                                                                                                                                                                                     Sequence 13247, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 16, 2004, 19:33:18 Job time : 50 secs
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35 AAAPVAVAAA 44
                                                                                                                                                                                       JS-09-815-242-13247
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

June 16, 2004, 19:23:53; Search time 20 Seconds (without alignments) 3246.464 Million cell updates/sec my on:

US-09-332-063-2 675 1 MPRAQPSSASYQPVPADPFA......KTPIQILGQBPDABMVEYLI 675 'itle: 'erfect score: 'equence:

OLIGO Gapop 60.0 , Gapext 60.0 coring table:

283366 seqs, 96191526 residues earched:

283366 otal number of hits satisfying chosen parameters: Ò Tord size :

inimum DB seq length: 0 aximum DB seq length: 2000000000

ost-processing: Listing first 45 summaries

PIR 78:*
1: Pir1:*
2: pir2:*
4: pir4:* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	sex-determining pr	acidic ribosomal p	hypothetical prote	hypothetical prote	dihydrolipoamide S	antifreeze protein			Φ	lal p	Ω,		ribosomal protein		ribosomal protein		riboso	omal	prot	ribosomal protein	0	ribosomal protein	probable ribosomal	ribosomal protein	Alu RNA-binding pr	signal recognition	acetyl-CoA carboxy	1 pro	pollen allergen pI
		ID	\$35568	RGUTP1	E87649	T21351	B55514	FDFLAW	S02326	A05161	I51125	H69091	R6DOP2	AD1106	AD1468	C95157	I40348	140350	AF3345	AC2817	D97595	H87310		R7HG12	A70615	S41123		S34196	4934	874	A38582
		DB	8	Н	~	~	~	ч	N	ď	~	N		2	n	7	7	~	~	~	Ŋ	N	N		C)	N	N	N	н	7	N
		Length	172	109	270	312	553	85	82	85	82	101	106	120	120	122	124	124	124	125	125	127	127	128	130	130	136	136	156	198	308
dР	Query	Match	1.8	1.6	1.6	1.6	1.6	1.5	1.5	1.5		1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	•	1.5		•	'n.	•	•	•	٠	÷,5	5.5
		Score	12	11	11	11	11	.0T	10	10	10	10	10	10	30	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	esult	No.	1 1	7	m	4	2	9	7	æ	σι	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote pyruvate dehydroge elastin precursor, chemotaxis protein ras GTease-activat fatty-acid synthas ribosomal protein ISU ribosomal protein probable ribosomal protein probable ribosomal protein probable protein probable protein hypothetical prote hypothetical prote probable LIM-domai hypothetical prote probable LIM-domai hypothetical prote
B99607 C82079 EABO 1C5047 3C1703 5C1703 5C9436 T77490 B7722 B97722 B97722 B97722 B87722 G68822 G70555
00000000000000000
315 635 747 762 850 102 102 111 111 111 1149 1149 1149 1200 220
111111 0000000000000000
6 11 6 12 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16

ALIGNMENTS

RESULT 1

835568 8ex-determining protein Sry - multimammate rat (Mastomys hildebrantii) C;Species: Mastomys hildebrantii C;Species: Mastomys hildebrantii C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Sep-1999 C;Accession: \$35568 R;Tucker, P.K.; Lundrigan, B.L. Nature 364, 715-717, 1993 A;Title: Rapid evolution of the sex determining locus in Old World mice and rats.	A;Reference number: S35565; MUID:93361118; PMID:8355784 A;Accession: S3556 A;Molecule type: DNA A;Residues: 1-172 <tuc></tuc>	A,Cross-references: GB:L29542; NID:g496161; PIDN:AAA40587.1; PID:g496162 (A)Genetios: Sry A,Gene: Sry A,Map position: Y	C.Superfamily: unassigned FWG box proteins; HMG box homology C.Keywords: DNA binding F;2-77/Domain: HWG box homology <hmgl></hmgl>	1.8%; Score 12; DB 2; Length 172; 100.0%; Pred. No. 0.017; tive 0; Mismatches 0; Indels 0; Gaps 0;
835568 Sex-determining protein Sry - multimamms Cispecies: Mastomys hildebrantii Cibate: 19-Mar-1997 #sequence_revision: CiAccession: 835568 R:Tucker, P.K.; Lundrigan, B.L. Mature 164, 715-717, 1993 Mature 164, 715-717, 1993	number: S35565; MUID:933611; S35568 Pe: DNA -172 <puc></puc>	.enceв: GB:L29542; NID:g496] n: Y	Ed E	Similarity 1 2, Conservati
S35568 sax-determining protein S C;Species: Mastomys hilde; C;Bate: 19-Mar-1997 #sequ. C;Accession: S35568 R;Tucker, P.K; Lundrigan Nature 364, 715-717, 1993	A; Reference number: S35 A; Accession: S3556 A; Molecule type: DNA A; Residues: 1-172 <tuc></tuc>	A, Cross-reference: C, Genetics: A, Gene: Sry A, Map position: Y	C;Superfamily: unassigne C;Keywords: DNA binding F;2-77/Domain: HMG box 1	Query Match Best Local & Matches 12

507 AAAAAAAAAA 518 153 AAAAAPAAAAP 164 셤 ઠે

RESULT 2

Accider ribosomal protein Pl - Trypanosoma cruzi
C;Species: 31-Bec-1992 #text_change 22-Jun-1999
C;Accession: 822644; 81924
R;Vazquez, M.P.; Schijman, A.G.; Levin, M.J.
R;Ference number: 822644; MJD99285148; PMID:1598221
A;Ference number: 822644
A;Ference number: 822644
A;Status: nucleic acid sequence not shown
A;Residues: 1-109 <VAZ.
A;Cross-references: EMBL:X65025; NID:g10629; FIDN:CAA46159.1; PID:g10630
C;Superfamily: rat acidic ribosomal protein Pl
C;Keywords: phosphoprotein; protein biosynthesis; ribosome

ö Gaps ô Query Match 1.6%; Score 11; DB 1; Length 109; Best Local Similarity 100.0%; Pred. No. 0.081; Matches 11; Conservative 0; Mismatches 0; Indels

Thu Jun 17 15:33:45 2004

507 AAAAAAAAA 517

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82 AAAAAAAAA 92

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A, Molecule type: DNA
A, Residues: 1-82 coll.
A, Cross-references: GB: M62412; GB: M62416; NID: G213592; FIDN: AAA49471.1; FID: G213593
A, Cross-references: GB: M62412; GB: M62416; NID: G213592; FIDN: AAA49471.1; FID: G213593
R; Davies, P.L.; Roach, A.H.; Hew, C.L.
Broc., Natl. Acad. Sci. U.S.A. 79, 335-339, 1982
A; Ritle: DNA sequence coding for an antifreeze protein precursor from winter flounder.
A; Reference number: A03194; MUID: 82197490; PMID: 6952188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antifreeze protein A - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: Pseudopleuronectes americanus (winter flounder)
C;Date: 30-58p-1989 #sequence_revision 30-58p-1989 #text_change 24-Oct-2000
C;Accession: S03256; JH0627
R;Scott, G.K.; Davies, P.L.; Kao, M.H.; Fletcher, G.L.
A; M.M.; Evol. 27, 29-35, 1988
A;Title: Differential amplification of antifreeze protein genes in the Pleuronectinae.
A;Reference number: S02326; MUID:88259236; PMID:3133486
                           A,Accession: B5514
A,Status: preliminary
A,Status: preliminary
A,Status: preliminary
A,Status: preliminary
A,Residues: 1-553 <HEL>
A,Cross-references: GB:U09865; NID:g497263; PIDN:AA21599.1; PID:g497265
A,Cross-references: GB:U09865; NID:g497263; PIDN:AA21599.1; PID:g497265
A,Cross-references: GB:U09865; NID:g497263; PIDN:AA21599.1; PID:g497265
A,Genetics:
A,Genetics:
A,Genetics: A,Genes: physicanide acetyltransferase; lipoyl/blotin-binding homology <LPB1>
F,6-78/Domain: lipoyl/blotin-binding homology <LPB2>
F,124-196/Domain: lipoyl/biotin-binding homology <LPB2>
F,526,530/Active site: H1s, Asp #status predicted
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C;Species: Pseudopleuronectes americanus (winter flounder)
C;Accession: J50704; A03194
R;Davies, P.L.
Gene 112, 163-170, 1992
A;Title: Conservation of antifreeze protein-encoding genes in tandem repeats.
A;Réference number: JH0627; MUID:92209995; PMID:1555765
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A, Residues: 1-82 < DA2>
A, Residues: 1-82 < DA2>
A, Experimental Source: clones 4-2b and 2A-7c
A, Note: the authors translated the codon AGC for residue 24 as Arg
C, Genetics:
A, Introns: 19/2
C, Superfamily: antifreeze protein
C, Keywords: antifreeze; plasma, tandem repeat
C, Keywords: antifreeze; plasma, tandem repeat
F, 1-21/Domain: propeptide #status predicted <SIG>
F, 22-44/Domain: propeptide #status predicted < PRO>
F, 45-B2/Product: antifreeze protein A #status predicted < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.6%; Score 11; DB 2; Length 553; Best Local Similarity 100.0%; Pred. No. 0.32; Matches 11; Conservative 0; Mismatches 0; Indels
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A; Reference number: A55514; MUID:94292470; PMID:8021225
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                                                                                                                                                                                                                                                                               Ypothetical protein CC3231 [imported] - Caulobacter crescentus

ypothetical protein CC3231 [imported] - Caulobacter crescentus

) Species: Caulobacter crescentus

) Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

) Accession: B87649

(Niverman, W.C.; Reldblyuw, TV.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

1, J.; Ermolaeva, W.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

1, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

1, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

1, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

1, J.; Ermolaeva, M.; White, O.; Salzberg, P.M.D:11259647

1, Molecule type: DNA
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);Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-May-2000

);Accession: B55514

**Accession: B55514

**Baccerio1: 176, 4334-4408, 1994

'Title: Biochemical and molecular characterization of the Alcaligenes eutrophus pyruvat
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submitted to the EMBL Data Library, September 1996
!/Reference number: 219411
!/Reference number: 219411
!/Recession: T21351
!/Status: preliminary; translated from GB/EMBL/DDBJ
!/Rolecule type: DNA
!/Rolecule type: DNA
!/Residues: 1-112 <WIL>
!/Experimental source: EMBL:279754; PIDN:CAB02098.1; GSPDB:GN00019; CESP:P25H2.10
!/Experimental source: clone F25H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V,Cross-references: GB:AE005673; NID:g13424915; PIDN:AAK25193.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iypothetical protein F25H2.10 - Caenorhabditis elegans
.?Species: Caenorhabditis elegans
.?Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
.?Accession: T21351
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Query Match 1.6%; Score 11; DB 2; Length 270; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 11; Conservative 0; Mismatches 0; Indels

1; Residues: 1-270 <STO>

1; Gene: CC3231 1, Genetics

602 APTPAPTPTPA 612

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84 APTPAPTPTPA 94

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Query Match
1.6%; Score 11; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 0; Indels

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i,Map position: 1 i,Introns: 49/1; 157/3 ;,Superfamily: rat acidic ribosomal protein P0

Genetics:

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Query Match
Best Local Si
Matches 10;
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;Molecule type: DNA
;Residues: 1-82 <DAV>
;Cross-references: GB:L00138; GB:J00929; NID:g343126; PIDN:AABS9964.1; PID:g457351
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*; Davies, P.I.
*; Davies, P.I.
*; Paris 112, 163-170, 1992
*; Paris 12, 163-170, 1992
*; Paris 12, 163-170, 1992
*; Paris 12, 163-170, 1992
*; Reference number: JH0627, MUID: 92209995; PMID: 1555765
*; Accession: JH0627
*; Residues: 1-82 - DMA
*; Residues: 1-82 - DMA
*; Cross-references: GB: M62415
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'Species: Pseudopleuronectes americanus (winter flounder)

'Abecies: Psep1996 #sequence_revision 13-Sep-1996 #text_change 24-Oct-2000

'Accession: I51125

'Pickett, M.; Scott, G.; Davies, P.; Wang, N.; Joshi, S.; Hew, C.

ur. J. Biochem. 143, 35-38, 1984

'Title: Sequence of an antifreeze protein precursor.

'Reference number: I51125

'Reference number: I51125

'Retexence number: I51125

'Retexus: preliminary; translated from GB/EMBL/DDBJ

'Residues: I-82 <PIC>

'Residues: I-82 <PIC>

'COSS = Teferences: GB:M28337; NID:G213581; PIDN:AAA49466.1; PID:G213582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ntifreeze protein B precursor - winter flounder
Species: Pseudopleuronectes americanus (winter flounder)
:Date: 05-Jun.1987 #sequence_revision 05-Jun-1987 #text_change 24-Oct-2000
:Accession: A05161
:Davies: 7-Li, Hudgh, C.; Scott, G.K.; Ng, N.; White, B.N.; Hew, C.L.
: Biol. Chem. 259, 9241-9247, 1984
:Reference number: A05161; MJID:84264559; PMID:6086629
V;Accession: S02326
V;Molecule type: DNA
V;Residues: 1-82 <SCO>
V;Cross-references: EMBL:X07506; NID:g64211; PIDN:CRA30389.1; PID:g64212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Best Local Similarity 100.
Matches 10; Conservative
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acidic ribosomal protein P2 - slime mold (Dictyostelium discoideum)

NyAlternate names: ribosomal phosphoprotein P2
C;Species: Dictyostellum discoideum
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: S14014
R;Priect, J; Candel, E; Coloma, A.
Nucleic Acids Res. 19, 1141, 1391
A;Title: Nucleotide sequence of a cDNA encoding acidic ribosomal phosphoprotein P2 in Di A;Reference number: S14014; MUID:9123921; PMID:1840653
A;Accession: S14014
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-106 <PRI: A;Accession: S14014
A;Coss-references: EMBL:X56192; NID:G7340; PIDN:CAA39655.1; PID:G7341
A;Accession: uncleotide sequence was submitted to the EMBL Data Library, November 1990
A;Note: the nucleotide sequence, including the amino end of the mature protein, was confir C;Superfamily: rat acidic ribosomal protein P2
C;Superfamily: rat acidic ribosomal protein P2
F;64-85/Region: alanine-rich
F;64-85/Region: alanine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                  Thosonal protein Lp1 - Methanobacterium thermoautotrophicum (strain Delta H)

Cispecies: Wethanobacterium thermoautotrophicum
Cispecies: Wethanobacterium thermoautotrophicum
Cispecies: Wethanobacterium thermoautotrophicum
Cispecies: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 13-Aug-1999
Ciscession: H69091
Rismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ciu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mac, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 199, 7135-7155, 1997
J. Rice of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Reterence number: A69000; MUID:98037514; PMID:9371463
A; Retsidues: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-101 cMTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:AE000926; GB:AE000666; NID:g2622806; FIDN:AAE86154.1; FID:g262281
A,Experimental source: strain Delta H
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Local Similarity 100.0%; Pred. No. 0.55;
tes 10; Conservative 0; Mismatches 0; Indels
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Ouery Match 1.5%; Score 10; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels
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C,Superfamily: rat acidic ribosomal protein Pl
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Matches 10; Conservative
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nson, T.; Hickey, E.K.; Holt, I.E.
A;Authors: Loftus, B.O; Yang, P.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A;Authors: Loftus, B.O; Yang, P.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C93157
A;Accession: C93157
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-12 ×GURA
A;Cross-references: GB:AE005672; PIDN:AAK75452.1; PID:g14972838; GSPDB:GN00164; TIGR:SP-A;Experimental source: strain TIGR4
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Gene 140, 137-138, 1994
Affilte: Sequences of the rplJL operon containing the L10 and L7/L12 genes from Brucella
A;Reference number: 140348; MUID:94171071; PMID:8125331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Brucella abortus
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change i3-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA-
A;Residues: 1-14 <RES.
A;Cross-references: GB:L19101; NID:G304270; PIDN:AAA19863.1; PID:G304271
C;Superfamily: Escherichia coli ribosomal protein L12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.5%; Score 10; DB 2; Length 122; Best Local Similarity 100.0%; Pred. No. 0.64; Matches 10; Conservative 0; Mismatches 0; Indels
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1.5%; Score 10; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels
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A;Gene: SP1354
C;Superfamily: Escherichia coli ribosomal protein L12
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                                                                                                                                       ribosomal protein L12 [imported] - Listeria innocua (strain Clip11262)
5/Species: Listeria innocua
6/Species: Listeria innocua
7/Species: Abech.
6/Species: Abech.
6/Spe
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]; Species: Streptococcus pneumoniae
]; Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
]; Accession: C95157
[; Tettelin, H., Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
]; J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:NC_003210; PIDN:CAD00778.1; PID:g16409616; GSPDB:GN00177 A;Experimental source: strain EGD-e
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4/Foatus: preliminary
4/Foatus: 1-120 cdla>
4/Cross-references: GB:AL592022; PIDN:CAC95516.1; PID:g16412712; GSPDB:GN00178
4/Experimental source: strain Clip11262
                     ribosomal protein L12 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels
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0.64;
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2,Superfamily: Bscherichia coli ribosomal protein L12
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idarity 100.0%;
Conservative 0
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Best Local Similarity
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(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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caulobacter
corynebacte
thermotoga
mycobacteri
homo sapien
pseudomonas
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675
1 MPRAQPSSASYQPVPADPFA.......KTPIQILGQEPDAEMVEYLI 675
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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RLA0_EIMTE
RLA0_EIMTE
ANDA_PSEAM
RL12_METTH
RL17_LISNO
RL17_CAUCH
RL17_THETH
RL17_CAUCH

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Gapop 60.0 , Gapext 60.0
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111 R.112_ARCFU 028780 archaeoglob 111 R.112_ARCFU 094949 aeropyrum p 111 R.112_ASPFU 094949 aeropyrum p 111 R.112_ASPFU 094949 aeropyrum p 1125 R.117_RICCN 092187 rickettsia 134 WZB_SALTI 092787 rickettsia 149 WZB_SALTI 092787 salmonella 092787 SALTI 092787 SALTI 092787 SALTI 09278 092787 SALTI 09278	TRYCE	159.1;
	TRYCR STANDARD; (43.) UG-1992 (Rel. 23, Created UG-1992 (Rel. 23, Last se COT-1996 (Rel. 34, Last se acidic ribosomal protein raycles, Buglenozoa; Kinetc "TaxID=5693; TENCE FROM N.A. INE-9228148; PubMed=1598 Heaz M., Schijman A., Levi Heoz M., Schijman A., Levi Heoz M., Schijman A., Levi Somal Pl type protein.; fied and this statement if ties requires a license a ties requires a license end an email to licenseen	A A A A A A A A A A A A A A A A A A A
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114 AA

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ODP2 ALCEU
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for conmercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60.8 acidic ribosomal protein P0.
RPA-0 OR F25H2.10.
Caenorhabditis elegans.
Ebkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                              Labbe M., Pery P.;
"Molecular cloning of a cDNA encoding an acidic ribosomal protein P2
60S acidic ribosomal protein P2.
Bimeria tenella.
Bukaryota, Alveolata, Apicomplexa, Coccidia, Bimeriida, Bimeriidae,
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                                                                                                                                                                                                                                                                    Score 11, DB 1, Length 114;
Pred. No. 0.039;
Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilkinson J.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                     114 AA; 11444 MW; 4C08C3C569078AA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                            311 AA.
                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                      1.6%; Score 11;
                                                                                                                                                                                                                     EMBL; AF353514; AAX38865.1; ALT INIT.
INCEPTED; INFO01813; Ribosomal 605.
Pfam; PF00428; 60s ribosomal in
Ribosomal protein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                   AAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                 NCBI_TaxID=5802;
                                                        STRAIN=PAPt38
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ID RLAO CAEEL
AC Q93572;
                                                                                                                                                                                                                                                     SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
115-MR-2004 (Rel. 43, Last annotation update)
Dibydrolipoamide acetyltransferase component of pyruvate dehydrogenase
complex (EC 2.3.1.12) (E2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overall
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MEDLINE-94292470; PubMed-8021225;
Hein S., Steinbuckhel A.;

Hein S., Steinbuckhel A.;

Listochemical and molecular characterization of the Alcaligenes eutrophus pyruvate dehydrogenase complex and identification of a new type of dihydrolipoamide dehydrogenase.";

J. Bacteriol. 176:4394-4408 (1994).

-i- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate dehydrogenase complex catalyzes the overall multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

-i- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = COA + S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyldihydrolipoamide.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 311; 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AA; 33642 MW; 2FA9A35CD24DE0F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553 AA.
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                                                                                                                                                                                                                                                                                                            EMBL, Z79754; CABO2098.1; -.
PIR; T21351; T21351.
Siena-2DPAGE; Q93572; --
WormPep; F25H2.10; CE09655.
InterPro; IPR001813; Ribosomal 60S.
InterPro; IPR001819; Ribosomal 60S.
InterPro; IPR00190; Ribosomal 1.10.
Pfan; PF00428; 60g_ribosomal_1.10.
Pfan; PF00468; Ribosomal_1.10; 1.
Ribosomal protein; Phosphorylation.
INIT_MST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 AAAAPAAAAP 285
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MEDLINE=92148833; PubMed=1738160;
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Matches 10; Conservative
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                                                                                                                                                                                        MEDLINE=95281060;
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                                                                                                                                                                                                                                                                       winter flounder.'
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                                                                                  mechanism
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P05394;
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RL12_METTH
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Davies P.L., Roach A.H., Hew C.-L.;
"DNA sequence coding for an antifreeze protein precursor from winter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    americanus).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scott G.K., Davies P.L., Kao M.H., Fletcher G.L.; "Differential amplification of antifreeze protein genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antifreeze protein A/B precursor.
Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Conservation of antifreeze protein-encoding genes in tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%; Score 11; DB 1; Length 553;
100.0%; Pred. No. 0.14;
ive 0; Mismatches 0; Indels
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BINDING 162 162 LIPOYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 526 POTENTIAL,
553 AA; 57338 MW; BF5D370CC60C3F12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A, 79:335-339(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-077-1986 (Rel. 02, Created)
23-077-1986 (Rel. 02, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AA.
                                                                                                   HSSP, Pl0862; IDPC.
InterPro: IPR010/78; ZOxoacid_dh.
InterPro: IPR0106256; AceF.
InterPro: IPR000089; Biotin lipoyl.
InterPro: IPR00016; Lipoyl_BS.
Pfam; PP00108; 2-oxoacid_dh; 1.
Pfam; PP00364; biotin lipoyl; 2.
Pr000m; PD01115; ZOxoacid_dh; 1.
PROSTE; PS001189; LIPOYL; Z.
send an email to license@isb-sib.ch)
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MEDLINE=84264559; PubMed=6086629;
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MEDLINE=88259236; PubMed=3133486;
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MEDLINE=92209995; PubMed=1555765;
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[5]
3D-STRUCTURE MODELING OF 45-81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Evol. 27:29-35(1988)
                                       EMBL, U09865, AAA21599.1; -. PIR, B55514; B55514, H5SP; P10802; IDPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT SITE
SEQUENCE
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NPA PSEAM
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                                                                                                                                                                                                                                                                                   Sicheri F., Yang D.S.C.; "Ice-binding structure and mechanism of an antifreeze protein from
Thou K.-C.;
Energy-optimized structure of antifreeze protein and its binding
                                                                                                                                                                                                                                                                                                                                                                                                  Nature 375:427-431(1995).
-!- FUNCTION: Antifreeze proteins lower the blood freezing point.
-!- MISCELANBOUS: The sequence shown is that of protein A.
-!- SIMILARITY: BELONGS TO THE TYPE-I APP PAMILY. TYPE I APP ARE
ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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115-JUL-1999 (Rel. 38, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
116-OCT-2001 (Rel. 40, Last annotation update)
118-OC xibosomal protein L12P ('A' type).
119-OR WHH1682.
119-OR WHH1682.
129-OR WH1682.
130-OC WHIPOPALOR (Methanobacteria) Methanobacteriales;
130-OC WHIPOPALOR (Methanobacteria) Methanobacteriales;
131-OC WHIPOPALOR (Methanobacteria) Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 10; DB 1; Length B2;
100.0%; Pred. No. 0.22;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7711 MW; C2AE7B74C0D46CC1 CRC64;
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S -> R (IN REF. 2).
                                                                                                                                                                                          K-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 45-81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L00138; AAB59964.1; -...
EMBL; L29178; AAB59964.1; -...
EMBL; M62414; AAA49469.1; -...
EMBL; M62414; AAA49469.1; -...
EMBL; M62416; AAA49471.1; -...
EMBL; M62416; AAA49471.1; -...
FMR; A05161; AAA49472.1; -...
FMR; A05161; A05161.
FMR; A05161; A05161.
FMR; A05162; S02126;
FMR; S02126; S02126;
FMR; S02126; S02126;
FMR; S03126; S02126;
FMR; S03176; S03100;
FMR; SMR; SMATIFREEZEI.
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                                                                                                                                                                                                                                  PubMed=7760940;
                                                                                                          J. Mol. Biol. 223:509-517(1992).
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01-AUG-1991 (Rel. 19, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DictyBase, DDB0001822; X56192.
InterPro; IPR001813; Ribosomal 60S.
Pfam; PP00428; 60S ribosomal; I.
Ribosomal protein; Phosphorylation.
                                                                                                                                                                                            EMBL; AF044919; AAC64512.1; --
InterPro; IPR001813; Ribosomal 60S.
Pfam; PF00428; 60g_ribosomal; I.
Ribosomal protein.
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MEDLINE=91232921; PubMed=1840653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60S acidic ribosomal protein P2.
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                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 10, Conservative
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Matches 10, Conservative
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RLAZ DICDI
ID RLAZ D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 626:162-169(1980).
-!- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation [By similarity].
-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linhart A., Piendi W.,
Submitted (JAN.1998) to the EMBL/GenBank/DDBJ database8.
-!-FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).
-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
                                                                                               Lee H.-M., Dubois J.,
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-81110590; PubMed-7006702;
Matheson A.T., Yaguchi M., Balch W.E., Wolfe R.S.;
Sequence homologies in the N-terminal region of the ribosomal 'A'
proceins from Methanobacterium thermoautotrophicum and Halobacterium
                                                             MEDELINE-9903514; PubNed=9371463;

MEDELINE-9903514; PubNed=9371463;

Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois of Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Luum W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Mann V., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltal: functional analysis and comparative genomics.";
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100.0%; Pred. No. 0.26;
ive 0; Mismatches 0; Indels
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Pfam, PR00428; 60s ribosomal; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 101 AA; 10480 MW; 6C1CEA3EF121FB85 CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
5-DS ribosomal protein L12P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus thermolithotrophicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000926; AAB86154.1; -.
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Les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                    FROM N.A.
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Matches
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-!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
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    -!- PTM: Phosphorylated.
    -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.

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"Nuclectide sequence of a cDNA encoding acidic ribosomal
phosphoprotein P2 in Dictyostelium discoideum.";
Nucleic Acids Res. 19:1341-1341(1991).
-!- FUNCTION: Plays an important role in the elongation step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 10; DB 1; Length 101;
100.0%; Pred. No. 0.26;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1,5%; Score 10; DB 1; Length 105; 100.0%; Pred, No. 0.27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AA; 10292 MW; 27262815729C8CB0 CRC64;
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Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MP. 00368; -; 1.
InterPro; IPR008932; Ribos_L12/7_oli
InterPro; IPR008932; Ribos_L12/7_oli
InterPro; IPR00826; Ribosomal_L12.
Probom; PD004326; Ribosomal_L12; 1.
TIGRFAMS; TIGR00855; L12; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae, and
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nes 10; Conservative 0
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                                                                                                      SEQUENCE PROM N.A.
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                                                           NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way anodified and this statement is not removed. Usage by and for commescial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:849-852 (2001).
-!- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                           Glaser P., Frangell L., Buchrieser C., Rusniok C., Amend A., Charbit A., Cherouani P., Chartwaler P., Chartwaler T., Cherouani P., Couve E., de Darnvar A., Dehoux P., Carbit A., Cherouani P., Couve E., de Darnvar A., Dehoux P., Entian K.-D., Fsihi H., Garcia-del Portillo F., Durant i., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautlier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst W., Kurn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicence J., Ng E., Nedjari H., Nordsisk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Raquez-Boland J.-A., Voss H., Wehland J., Cossart P., "Comparative genomics of Listeria species."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
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                                                                                                                                                                                                                                Listeria innocua.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
VODI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TLURVOOD, DOOD, RIBOSOMA! Drotein; Complete proteome.
Ribosomal protein; Complete proteome.
12441 MW; 21C447DF78F79138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RI7 LISMO STANDARD; PRT; 120 AA. 08YĀA3; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 50S ribosomal protein L7/L12.
                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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InterPro; IPR008932; Ribos L12/7 olig.
InterPro; IPR000206; Ribosomal L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00542; Ribosomal L12; 1.
ProDom; PD001326; Ribosomal L12; 1.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar 6a,
MEDLINE-21537279; Pubmed=11679669;
                                                                                             28-F5B-2003 (Rel. 41, Created) 28-F5B-2003 (Rel. 41, Last seq. 28-F5B-2003 (Rel. 41, Last seq. 505 ribosomal protein L7/L12. RPLL OR LIN0283.
                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; ALS96164; CAC95516.1; -. PIR; AD1468; AD1468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO0855; L12; 1
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ListiList, LIND0283; -.
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SEQUENCE FROM TO SELVINE SECURITY SEQUENCE FROM TO SEQUENCE FROM TO SEQUENCE FROM THE SECURITY SEQUENCE AS GLESCH SECURITY SEQUENCE TO SEQ
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100.0%; Pred. No. 0.3;
ive 0; Mismatches 0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein; Complete proteome.
SEQUENCE 120 AA; 12469 MW; 8EC3DE417F6E1954 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S riboscmal protein 17/L12.
RPLL OR SP1354 OR SPR1211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AA
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MEDLINE=21357209; PubMed=11463916;
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RESULT 10 RL7_LISMO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 2586;

MEDLINE-186594; PubMed=1889109;

MEDLINE-186594; PubMed=11889109;

MEDLINE-186594; PubMed=11889109;

Majarral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Bhattacharyya A., Bartman A., Gardher W., Grechkin G., Zbu L.,

Majarea O., Chu L., Kogan Y., Chaga O., Goltsman E., Berral A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Ponstein M., Kyrpides N., Overbeek R.;

Ponstein M., Kyrpides N., Overbeek R.;

Thenome sequence and analysis of the oral bacterium Fusobacterium

nucleatum strain ATCC 25586 "",

J. Bacteriol. 184:2005-2018 (202).

-!-FUNGTON: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).

-!- SIMILARITY: Belongs to the Li2P family of ribosomal proteins.
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Pred. No. 0.31;
                                                                                                                                                                                                                      rusowacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF00542; Ribosomal L12; 1.
Pr00Dom; PD001326; Ribosomal L12; 1.
TIGREAMS; TIGR00855; L12; 1.
Ribosomal proctein; Complete proteome.
SEQUENCE 122 AA; 12605 MW; 4382328A2E266BA3 CRC64;
                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
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InterPro; IPR008932; Ribos L12/7 olig-
InterPro; IPR000206; Ribosomal L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE010507; AAL94122.1; -.
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NCBI_TaxID=29459, 29461, 235;
                                                                                                                                                                 50S ribosomal protein L7/L12. RPLL OR FN2037.
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Best Local Similarity 100.
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Brucella abortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=76856;
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam I.A., White O., Salberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey B.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC EAA-255 / R6;
MEDLINE=2142945; PubMed=11544334;
MEDLINE=2142945; PubMed=11544334;
MEDLINE=2142945; PubMed=11544334;
DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Glimour R., Glass J.S., Khola H., Kraft A.R., Legace R.E.,
McAnen S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Nortis F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
Sun P.-M., Winkler M.E., Yang Y., Young-Pellido M., Zhoo G.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-42.

MEDILINE=9177772; PubMed=9025278;

MEDILINE=9177772; PubMed=9025278;

MEDILINE=9177772; PubMed=9025278;

MODICIONAL ARTIDOGUE B.A., LODGE R., Sletten K.;

"MODICIONAL ARTIDOGUE B.A., LODGE R., Sletten K.;

"MODICIONAL ARTIDOGUE B.A., LODGE R., Sletten K.;

MICROPIOLOGY 143:55-61(1997).

-!- FUNCTION: Seems to be the binding site for several of the factors incolved in protein synthesis and appears to be essential for accurate translation (By similarity).

-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18s J.I.;
snowe of the bacterium Streptococcus pneumoniae strain R6.";
Bacteriol. 183:5709-5717(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 10; DB 1; Length 121;
100.0%; Pred. No. 0.3;
tive 0; Mismatches 0; Indels
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THAMAP; MF 00368; -; 1.

INTERPO: JPR008932; Ribos_L12/7 olig.

INTERPO: JPR000206; Ribosomal_L12.

Pfam; PF00542; Ribosomal_L12; 1.

TIGRPAMS; TIGR00855; L12; 1.

Ribosomal protein; Complete proteome.

INIT_MET
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EMBL; AE008493; AAL00015.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                       Science 293:498-506(2001)
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               pneumoniae.";
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=B.melitensis; STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=94357413; PubMed=8076798;
                                                                                                                                                                                              PRT; 124 AA
RESULT 13
RL7 BRUMB
RL7 BRUMB
AC P4110
DT 01-FE
DT 28-FE
DT 28-FE
DS SOS R
GN BRUCE
OS BRUCE
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122 AA.

PRT;

STANDARD;

RESULT 12 RL7_FUSNN ID_RL7_FUSNN

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Gaps

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0; Indels

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Section 6. Section and municocide coquence of Studella melitensis 17/112

Tibescan] Procedin., Ser. 120:127-240(1994).

Section 2. Section and municocide coquence of Studella melitensis 17/112

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NEDLINES-1060850; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsan I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Giller W., Grant C.,

Kutyavin T., Levy R., Ei M. J., McClelland B., Palmieri A.,

Kaymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last amotation update)
28-FEB-2003 (Rel. 41, Last amotation update)
50s ribosomal protein L7/L12.
RPLL OR ATU1957 OR AGR C 3571.
Agrobacterium tumefacieins (Exrain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobiaum/Agrobacterium group; Agrobacterium.
NCBI TaxID=176299;
                                                                                        1.5%; Score 10; DB 1; Length 124;
100.0%; Pred. No. 0.31;
tive 0; Mismatches 0; Indels
                                             104 104 "K -> N (IN REF. 5).
124 AA; 12546 MW; A56E1079AA8BE7F4 CRC64;
           TIGRPAMs, TIGRO0855, L12; 1.
Ribosomal protein; Complete proteome.
CONFLICT 104 K -> N K
ProDom; PD001326; Ribosomal L12; 1.
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EMBL; AE008114; AAK87717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2317-2323(2001).
                                                                                                        Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                       500 AAAPVAVAAA 509
                                                                                                                                                                                     34 AAAPVAVAAA 43
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PIR; D97595; D97595.
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                                                              SEQUENCE
                                                                                            Query Match
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RL7_AGRT5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the ENEL outstation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-entities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 7:331-338(2000).
-!- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).
-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                 1.5%; Score 10; DB 1; Length 125; 100.0%; Pred. No. 0.31; tive 0; Mismatches 0; Indels
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HAMAP; MF_00368; -; 1.
InterPro; IPR008932; Ribos_L12/7 olig.
InterPro; IPR008932; Ribosomal_L12.
InterPro; IPR00842; Ribosomal_L12; 1.
ProDom; PD001326; Ribosomal_L12; 1.
TIGREPMS; TIGR0855; L12; 1.
TIGREPMS; TIGR0855; L12; 1.
SIDOSOMAl Protein; Complete proteome.
SEQUENCE 125 AA; 12736 MW; 37A8E027PE77175D CRC64;
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InterPro; IPR008932; Ribos L12/7 olig.
InterPro; IPR0020505; Ribos mal L12.
Profiler, PR00542; Ribosomal L12; 1.
Profiler, PR001326; Ribosomal L12; 1.
IIGRAPANS; TIGR00855; L12; 1.
RIBOSOMAI DIOCEGIN, COMPLETE Profeome.
SEQUENCE 125 AA; 12735 MM; 98814454212A55AF CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SOS Tibosomal protein L/L12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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Best Local Similarity 100.
Matches 10; Conservative
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ALT RHILO
ID RLT RHILO
AC Q998N67;
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Gaps

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Search completed: June 16, 2004, 19:26:11 Job time : 18 secs

us-09-332-063-2.oli.rag

Abg54477 Abg42601 Aau69439 Abp69085 Adc38518

Human pep Human pur Human pol Human AML Human ang Mouse Jun Human pol Human ORP Human ORP Human pro A polyala Antigen t Novel hum Winter fl

Adc37654 Abr56262 Abu70751

Aam93770 F Abg97502 H Abr56263 N Aab17657 H Adc37657 A Aab2225 A Aaw32225 A Aaw3225 A Aaw3225 A Aaw3237 M Abo00600 N Aay23877 W

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kringle domain; anglostatin; plasminogen receptor;
anglogenesis-related disease; tumor; diabetes; rheumatoid arthritis;
inflammatory disease; psoriasis; chronic inflammation; intestine; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human angiogenesis-associated protein which is able to bind an N-terminal fragment of plasminogen. The protein is designated ABP-1, and binds the first 4 kringle domains (K1-K4) and/or kringle 5 (K5) of plasminogen. These four kringle domains comprise angiostatin. The protein acts as a receptor for plasminogen. The angiostatin-binding domain of the ABP-1 protein is described in AAY54054. A polymorphic variant of ABP-1 is also described, in AAY54053. ABP-1 can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human protein useful for treating angiogenesis associated diseases
                                                                                                                                                                                                                                                                          angiogenesis-associated protein; plasminogen; ABP-1;
                                                                                                                                                                                                                                                           An angiogenesis-associated protein which binds plasminogen.
                                                                                                                                                                        ALIGNMENTS
                       ABG42601
AAU69439
                                     ABP69085
ADC38518
ADC38518
ADC37654
ABR56262
ABW93770
AAM93770
ABR56263
AAB81861
AAB92866
AAB92866
AAB92866
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ABO00600
AAY23877
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                                                                                                                                                                                                                                                                                                                                                                                     98SE-00002130.
98US-0089266P.
98SE-00004372.
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                 (first entry)
obesity; gene therapy
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N-PSDB; AAZ45329.
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17-DEC-1998;
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AAY54052;
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 An anglog
A variant
Human CGD
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Peptide #
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                                                   2004, 19:15:43; Search time 61 Seconds (without alignments) 3126.550 Million cell updates/sec
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                                                                                   US-09-332-063-2
675
1 MPRAQPSSASYQPVPADPFA......KTPIQILGQBPDAEMVEYLI
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- 2004 Compugen Ltd
                                                                                                                                                                        otal number of hits satisfying chosen parameters:
                                                                                                                                          1586107 seqs, 282547505 residues
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                                       protein - protein search, using sw model
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ABP43965
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genesemp2003bs:*
        GenCore
Copyright (c) 1993
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geneseqp1990s:*
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laximum DB seq length: 200000000
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Match Length
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be used to manufacture medicaments for treating angiogenesis-related diseases or disorders, such as tumor conditions, diabetes, rheumatoid arthritis, and even some inflammatory diseases such as psoriasis, chronic inflammation of the intestine, asthma, etc. . The protein may also be able to treat and cure, or prevent, obesity. The ABP-1 DNA can be used in gene therapy techniques
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                                                                                                                                                                                                                                                                                                                                  SEDTRKTI SQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKL
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                                                                                                                                     675;
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                                                                                                                                Score 675; DB 3;
Pred. No. 0;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 675; Conservative
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AAYS4053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a polymorphic variant of a human angiogenesis-associated protein which is able to bind an N-terminal fragment of plasminogen. The native protein, described in AMYS4052, is designated ABP-1, and binds the first 4 kringle domains (X1-K4) and/or kringle 5 (K5) of plasminogen. These four kringle domains comprise angiostatin. The ABP-1 protein acts as a receptor for plasminogen. The angiostatin-binding domain of the ABP-1 protein is described in AAX54054. ABP-1 can be used to manufacture medicaments for treating angiogenesis-related diseases or disorders, such as turnor conditions, diabetes, rheumatoid arthritis, and even some inflammatory diseases such as portein any also be able to treat and cure, or prevent, obesity. The ABP-1 protein may also be able to treat and cure, or prevent, obesity. The ABP-1 protein may also be able to treat and cure, or prevent, obesity. The ABP-1 protein may also be able to treat and cure, or prevent, obesity. The ABP-1 protein may also also as a protein and cure, or prevent, obesity.
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kringle domain; angiostatin; plasminogen receptor;
angiogenesis-related disease; tumor; diabetes; rheumatoid arthritis;
inflammatory disease; psoriasis; chronic inflammation; intestine; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis associated diseases
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//note= "these residues are either Glu-Leu-Ala
Prote= "these residues are either Glu-Leu-Ala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human protein useful for treating
                                                                                                                                             /label= Asn, Ser, Asp
                                                                                                               Location/Qualifiers
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98US-0089266P.
98SE-00004372.
98US-0114386P.
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                                                   obesity; gene therapy
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                                                                                                                                                              Misc-difference
                                                                                                                                 Misc-difference
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29-DEC-1998;
                                                                                  Homo sapiens
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The present invention relates to novel cell growth, differentiation and death (CGDD) proteins and polymucleotides encoding them. The sequences of the invention are useful in diagnosing, preventing and treating disorders associated with an abnormal expression or activity of CGDD such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), meacular disorders (e.g. quiabetes; Grave's disease), Alzheimer's endocrine disorders (e.g. diabetes; Grave's disease), caractronia), endocrine gisorders (e.g. diabetes; Grave's disease), gastrofinestinal scleorderma, eystemic lugus arythematosus, allerques), gastrofinestinal disorders (e.g. Goodpasture's syndrome), infections (e.g. viral) bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis) cand hepatic diseases (e.g. cirrhosis). The polymucleotides can be used to create humanised animals or transgenic animals to model human diseases.

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Sequence 993 AA; CGDD-7 protein

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570
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                                                             451 RDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATAAATITTTWVAAAPVAVAAAA 510
                                                                                                              511 APAAAAAAAAYOVAPAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAAAAPAFFV 570
                                                                                                                                                                       SHSSTLTGSPIMEBKRDDKSWKGSLGILLGGDYRABYVPSTPSPVPPSTPLLSAHSKTGS 450
                                                                                                                                                      PAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPAVAQAEVPASPATGPGPHR 630
                                                                                                                                                                                                                                                                                                                                                                                                                       Human, cell growth, differentiation and death protein; CGDD; leukaemia; neurodegenerative disorder; Parkinson's disease; Alrheimer's disease; muscular disorder; myotonic dystrophy; catatonia; endocrine disorder; diabetes; drave's disease; cancer; immunological disorder; scleroderma; systemic lupus erythematosus; allergy; Crohn's disease; renal disorder; gastrointestinal disorder; doodpasture's syndrome; infection, cirthosis; cardiovascular disorder; doodpasture's syndrome; infection, cirthosis; transgenic animal; gene therapy; neuroprotective; relaxant; cyrostatic; dermatological; immunosuppressive; cerebroprotective; anticonvulsant; antibacterial; antibarassitic; fungicide; virucide; uropathic; cardiant;
                                         RDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATAATITTTWVAAAPVAVAAAA
                                                                                                APAAAAAPSPATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAVQVAPAAPAVV
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2001US-0342761P.
2002US-0349705P.
2002US-0354764P.
2002US-0356216P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protozoacide; nootropic
                                                                                                                                                                                                                                                                                                                                                                                             Human CGDD-7 protein.
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20-DEC-2001; 2
15-JAN-2002; 2
06-FEB-2002; 2
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72.9%; Score 492; DB 7; Length 993; 106.0%; Pred. No. 0; Live 0; Mismatches 0; Indels
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                                                                           Matches 492; Conservative
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                                     Local Similarity
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A, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
P, Baughn MR, Gorvad AB, Yue H, Lee EA, Becha SD, Tang YT;
Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
Y. Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
D, Blake JJ, Ho A, Zheng W;

Griffin .. Marquis JP, barkar A, Tran UK, Swarnakar A, Traque WW, Lee SY, Khar

WPI; 2003-532903/50. N-PSDB: AAD57227

(INCY-) INCYTE GENOMICS INC

New CGDD polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of CGDD, e.g. neuromuscular, immunological, cardiovascular disorders, cancer

Claim 1; Page 220-222; 299pp; English

e.g. nel

616

557 AAAVQVAPAAPAPVPAPALVPVPAPAAQASAPAQTQAPTSAPAVAPTPAPTPTPAVAQA

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                                                                                                                                                                                                                                                                                                                                                The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnerary, neuroprotective, immunomodulator, cytostatic and antiniflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcars, Alzheimer's disease, Muntington's disease, amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABB4354-ABB4399 represent polypeptides encoded by polynucleotides of the invention. WOTEs The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KSLMSISNAGSGLLGHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THVAAAAPVAVAAAAAAAAAAAAAABSPATAAATAAAVSPAAAGQIPAAASVASAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 MOQALVQLQAACEKREQLEHRLRTRLERELESLRIQQRQGNCQPTNVSEYNAAALMELLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 EKEERILALEADMTKWEOKYLEENVWRHFALDAAATVAAQRDTTVISHSPNTSYDTALEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSIMSISNAGSGILSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSTPLLSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVAAAATAAAITATTTT
                                                                                                                                                                                                                                                                New polypeptides and their encoded proteins, useful as mutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
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ulcer, Alzheimer's disease, Huntington's disease,
amyotrophic lateral sclerosis; autoimmune disorder; inflammation,
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                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID # 868; 357pp + Sequence Listing; English.
                                                                                                                                                                                            Zhao QA,
                                                                                                                                                                                          Asundi V, Zhang J,
F, Drmanac RT;
                                                                                                                     11-OCT-2001; 2001WO-US027760.
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                                                                                                                                             12-OCT-2000; 2000US-00687527
                                                                                                                                                                                          Zhou P,
Wehrman
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Best Local Similarity 100.
Matches 479; Conservative
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N-PSDB; ABQ61209.
                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                          Liu C,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 479 AA;
                                                                     WO200231111-A2
                                                                                                                                                                                                                                                                                                     inflammation.
                                               Home sapiens
                                                                                              18-APR-2002
                        vulnerary
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Xue AJ,
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cand in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders or polypeptide and polymucleotide sequences have applications in dispositics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess bliodiversity responsible for genetic disorders or other traits to assess bliodiversity responsible for genetic disorders or other traits to assess bliodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed sequences.
361 AAAVQVAPAAAAPAPVPAPALVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAFTPTPAVAQA 420
                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #17950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2006US-00540217.
23-AUG-2000; 2006US-00649167.
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us-09-332-063-2.oli.rag

Sequence 143 AA;

X X

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The present sequence represents the angiostatin-binding domain, designated Big-3, of a human angiogenesis-associated protein. The protein binds an N-terminal fragment of plasminogen. The ABP-1 protein is designated ABP-1, and binds the first 4 kringle domains (KI-K4) and/or kringle 5 (K5) of plasminogen. These four kringle domains comprise angiostatin. The ABP-1 protein acts as a receptor for plasminogen. A polymorphic variant of ABP-1 is also described, in AAY54083. ABP-1 can be used to manufacture medicaments for treating angiogenesis-related diseases or disorders, such as tumor conditions, diabetes, rheumatoid arthritis, and even some inflammatory diseases such as psoriasis, chronic inflammation of the intestine, asthma, etc. The protein may also be able to treat and cure, or prevent, obesity. The ABP-1 DNA can be used in gene therapy techniques
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                                                                           584
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                                                                                                                                                                        180
                                                                                                                                                                                        SEDTRKTISQLFAKNKESQREKEKLEABLATARSTNEDQRRHIEIRDQALSNAQAKVVKL 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human protein useful for treating angiogenesis associated diseases or disorders.
                                                                    1 MPRAQPSSASYQPVPADPPAIVSRAQQMVEILSDENRNLRQELEGCYEKVARLQKVETEI
                                                                                                           QRVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKBYEG
                                                                                                                                                                        SEDTRKTISQLFAKNKESQREKEKLEAELATARSTWEDQRRHIEIRDQALSNAQAKVVKL
                  Gaps
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                Indels
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 Pred. No. 8.5e-157;
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                Mismatches
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98US-0089266P.
98SE-00004372.
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100.08;
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                Conservative
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Best Local Similarity
                                                                                                                                                                                                                                      EEE 183
                                                                                                                                                                                                                                                                    EEE 707
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17-DEC-1998;
29-DEC-1998;
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                Matches 183;
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                                                          ESNKTAAVAPISVPAPVAAAATAAAITATAATITTIMVAAAPVAVAAAAAAAAAPSPA 521
                                                                                                                      522 TAAATAAAVSPAAAGQIPAAASVASAAAAVAPSAAAAAAVQVAPAAPAPVPAPALVPVPAP 581
                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                       9
                                                                                 1 ESINITAAVAPISVPAPVAAATAAAITATAATITTIMVAAAPVAVAAAAAAAABSPA
                                                                                                                                                                                                                                                                                                                                                                                     Peptide #3180 encoded by probe for measuring cervical gene expression.
                              Gaps
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                             ö
 Length 143;
                             0; Indels
Query Match 21.2%; Score 143; DB 3; Lf Best Local Similarity 100.0%; Pred. No. 3.7e-121; Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 21572; 487pp; English
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                                                                                                                                                                                  AAAQASAPAQTQAPTSAPAVAPT
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                    12-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                cervical cancer.
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21-SEP-2000;
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   Query Match
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RESULT 8

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Seguence 208 AA;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                               Homo sapiens.
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                       17-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exor nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 genome-derived single exon nucleic acid probes useful for analyzing expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                     Gaps
                                                                                                                                                                                                                                                        foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 MPRAQPSSASYQPVPADPFAIVSRAQQMVEILSDENRNIRQELEGCYEKVARLQK 208
                                                                          154 MPRAQPSSASYQPVPADPFAIVSRAQCMVEILSDENRNLRQELEGCYEKVARLQK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPRAQPSSASYQEVPADPFALVSRAQQMVEILSDENRNLRQBLEGCYEKVARLQK 55
                                                             1 MPRAQPSSASYQPVPADPPAIVSRAQQMVEILSDENRNIRQELSGCYBKVARLQK
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                                     ő
                                                                                                                                                                                                                               Peptide #3238 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 28367; 639pp + Sequence Listing; English.
          Length 208;
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                                  Indels
 DB 4; heus
1, 3.4e-41;
0;
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100.0%; Pred. No. 3.4e-41;
iive 0; Migmatches 0;
8.1%; Scor.
100.0%; Pred. No. J...
7. 0; Mismatches
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                                                                                                                                                    ABB35732 standard; peptide; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-00632366,
2000US-0234687P,
2000US-0236359P,
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0060840B.
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                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 55; Conservative
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483447/52
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 208 AA;
                                                                                                                                                                                                                                                                                                         WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                      04-FEB-2002
                                                                                                                                                                                                                                                                                  Homo sapiens
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          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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AAM29234
ID AAM2
XX
AC AAM2
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for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; microarray; single exon probe; gene expression; breast; disease;
Peptide #3271 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 MPRAQPSSASYQPVPADPPAIVSRAQQMVBILSDENRNIRQBLBGCYEKVARIQK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPRAQPSSASYQPVPADPPAIVSRAQQMVBILSDENRNLRQELEGCYEKVARLOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                          Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%; Score 55; DB 4; Le
100.0%; Pred. No. 3.4e-41;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W, Rank DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                             2000US-0180312P.
2000US-020446P.
2000US-00608408.
2000US-023368.
2000US-023468TP.
2000US-023468TP.
2000GS-023468TP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from human placenta. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein #3157 encoded by probe for measuring heart cell gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPRAQPSSASYQPVPADPFAIVSRAQQMVBILSDENRNLRQELEGCYEKVARLQK 55
                                                                                                                                                                                                                                                                                                                          New spatially-addressable set of single exon nucleic acid probes, for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 13535; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression; heart; microarray; vascular system;
lar disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.1%; Score 55; DB 4; Length 208; Best Local Similarity 100.0%; Pred. No. 3.4e-41; Matches 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB21158 standard; protein; 208 AA
                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                 03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
2-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                         26-MAY-2000; 2000US-0207456P.
                       2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          congenital heart disease.
                                                                                                                                                                                                                                                                                   WPI; 2001-496933/54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                         Penn SG,
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The present invention relates to single exon mucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA13135). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPRAQPSSASYQPVPADPFAIVSRAQQMVEILSDENRNLRQELBGCYEKVARLQK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed probe encoded protein SEQ ID NO: 29229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma.
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8.1%; Score 55; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.4e-41;
Matches 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         Claim 15; SEQ ID NO 22928; 530pp; English.
                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM68923 standard; protein; 208 AA.
04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0204465F.
30-UJX-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234659P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i6-MAY-2000; 2000US-0207456P.
i0-JUN-2000; 2000US-00608408.
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21-SEP-2000; 2000US-0234687P
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                                                                                                                                                                     Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 208 AA;
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                                                                                                                                                                     Penn SG,
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(MOLE-) MOLECULAR DYNAMICS INC

30-JAN-2001; 2001WO-US000666

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Rank

Cher W,

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and cayeloma. The present sequence is a protein encoded by one of the probes of the invention
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                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, brain expressed exon, gene expression analysis; probe, microarray;
Alzheimer's disease, multiple sclerosis; schizophrenia, epilepsy, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain expressed single exon probe encoded protein SEQ ID NO: 28646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human brains.
                                                                                                                                                                                                                                                                                                                                                                                                         1 MPRAQPSSASYQPVPADPFAIVSRAQQMVEILSDENRNLRQELEGCYEKVARLQK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 28646; 650pp + Sequence Listing; English.
                                                                                                                                 Example 4; SEQ ID NO 29229; 658pp + Sequence Listing; English
                                                                                                gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM56541 standard; protein; 208 AA
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30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632866.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345897P.
04-OCT-2000; 2000GS-00024263.
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Witches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52
                                                WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                      Sequence 208 AA;
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                 SG
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                   Penn
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(first entry)

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Chen W, Rank

2000US-0180312P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
ij
                                                                                                   Gaps
                                                                                                                                                   154 MPRAQPSSASYQPVPADPFAIVSRAQQMVEILSDENRNLRQBLBGCXBKVARLQK 208
                                                                                                                                55
The present sequence is a protein encoded by
                                                                                                                                  1 MPRAQPSSASYOPVPADPFAIVSRAQOMVEILSDENRNLRQELEGCYEKVARLQK
                                                                                                                                                                                                                                                                                                                                                      Human, liver, cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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                                                                       Length 208,
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                                                                        DB 4; L
3.4e-41;
                                                                       8.1%; Score 55; DB 100.0%; Pred. No. 3.4 ive 0; Mismatches
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                              Human liver peptide, SEQ ID No 29236
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                                                                                                                                                                                                                                         ABG50588 standard; peptide; 208
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-02363359P.
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               the probes of the invention
                                                            Query Match
Best Local Similarity 100..
Thes 55; Conservative
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cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                              Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157273-A2
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21-SEP-2000;
27-SEP-2000;
 and
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                                                                                                                                                                                                                                                                     ABG50588;
   epilepsy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe, human, breast disease, breast cancer, development disorder, inflammatory disease, proliferative breast disease, non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                              154 MPRAQPSSASYQPVPADPPAIVSRAQOMVEILSDENRNIRQELEGCYEKVARLQK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #3145 encoded by probe for measuring breast gene expression.
                                                              1 MPRAQPSSASYQPVPADPPAIVSRAQQMVBILSDENRNLRQELEGCYEKVARLQK 55
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0; Indels
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                                                                                                                                                                                                                                                                                    AAM04463 standard; protein; 208 AA.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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Best Local Similarity 100.0
Matches 55; Conservative
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